

SEQUENCE LISTING

(1) GENERAL INFORMATION:

(i) APPLICANT: Koziel, Michael G.
Desai, Nalini M.
Lewis, Kelly S.
Kramer, Vance C.
Warren, Gregory W.
Evola, Stephen V.
Crossland, Lyle D.
Wright, Martha S.
Merlin, Ellis J.
Launis, Karen L.
Rothstein, Steven J.
Bowman, Cindy G.
Dawson, John L.
Dunder, Erik M.
Pace, Gary M.
Suttie, Janet L.

(ii) TITLE OF INVENTION: SYNTHETIC DNA SEQUENCE HAVING ENHANCED
INSECTICIDAL ACTIVITY IN MAIZE

(iii) NUMBER OF SEQUENCES: 94

(iv) CORRESPONDENCE ADDRESS:

(A) ADDRESSEE: Syngenta Biotechnology, Inc.
(B) STREET: 3054 Cornwallis Road
(C) CITY: Research Triangle Park
(D) STATE: NC
(E) COUNTRY: USA
(F) ZIP: 27709

(v) COMPUTER READABLE FORM:

(A) MEDIUM TYPE: Floppy disk
(B) COMPUTER: IBM PC compatible
(C) OPERATING SYSTEM: PC-DOS/MS-DOS
(D) SOFTWARE: PatentIn Release #1.0, Version #1.30

(vi) CURRENT APPLICATION DATA:

(A) APPLICATION NUMBER:
(B) FILING DATE:
(C) CLASSIFICATION:

(vii) PRIOR APPLICATION DATA:

(A) APPLICATION NUMBER: US 09/547,422
(B) FILING DATE: 11-APR-2000

(vii) PRIOR APPLICATION DATA:

(A) APPLICATION NUMBER: US 08/459,504
(B) FILING DATE: 02-JUN-1995

(vii) PRIOR APPLICATION DATA:

(A) APPLICATION NUMBER: US 07/951,715
(B) FILING DATE: 25-SEP-1992

(vii) PRIOR APPLICATION DATA:

(A) APPLICATION NUMBER: US 07/772,027
(B) FILING DATE: 04-OCT-1991

(viii) ATTORNEY/AGENT INFORMATION:
 (A) NAME: Meigs, J. Timothy
 (B) REGISTRATION NUMBER: 38,241
 (C) REFERENCE/DOCKET NUMBER: S-18805I

(ix) TELECOMMUNICATION INFORMATION:
 (A) TELEPHONE: (919)541-8587
 (B) TELEFAX: (919)541-8689

(2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 3468 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: *Bacillus thuringiensis kurstaki*
 (B) STRAIN: HD-1

(ix) FEATURE:
 (A) NAME/KEY: misc_feature
 (B) LOCATION: 1..3468
 (D) OTHER INFORMATION: /product= "Full-length native
 cryIA(b)"
 /note= "Appears in Figures 1 and 4 as BTHKURHD."

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

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GAACAGTTAA TTAACCAAAG AATAGAAGAA TTCGCTAGGA ACCAAGCCAT TTCTAGATTA	300
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GGCAACTATA CAGATCATGC TGTACGCTGG TACAATACGG GATTAGAGCG TGTATGGGGA	660
CCGGATTCTA GAGATTGGAT AAGATATAAT CAATTTAGAA GAGAATTAAC ACTAACTGTA	720
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ATAATGGCTT CTCCTGTAGG GTTTTCGGGG CCAGAATTCA CTTTCCGCT ATATGGAAC	1020
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GCGATGATTC ATGCGGCAGA TAAACGCGTT CATAGCATTC GAGAAGCTTA TCTGCCTGAG      2760
CTGTCTGTGA TTCCGGGTGT CAATGCGGCT ATTTTGAAG AATTAGAAGG GCGTATTTTC      2820
ACTGCATTCT CCCTATATGA TGCGAGAAAT GTCATTAAAA ATGGTGATTT TAATAATGGC      2880
TTATCCTGCT GGAACGTGAA AGGGCATGTA GATGTAGAAG AACAAAACAA CCACCGTTCG      2940
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CGTGGCTATA TCCTTCGTGT CACAGCGTAC AAGGAGGGAT ATGGAGAAGG TTGCGTAACC      3060
ATTCATGAGA TCGAGAACAA TACAGACGAA CTGAAGTTTA GCAACTGTGT AGAAGAGGAA      3120
GTATATCCAA ACAACACGGT AACGTGTAAT GATTATACTG CGACTCAAGA AGAATATGAG      3180
GGTACGTACA CTTCTCGTAA TCGAGGATAT GACGGAGCCT ATGAAAGCAA TTCTTCTGTA      3240
CCAGCTGATT ATGCATCAGC CTATGAAGAA AAAGCATATA CAGATGGACG AAGAGACAAT      3300
CCTTGTGAAT CTAACAGAGG ATATGGGGAT TACACACCAC TACCAGCTGG CTATGTGACA      3360
AAAGAATTAG AGTACTTCCC AGAAACCGAT AAGGTATGGA TTGAGATCGG AGAAACGGAA      3420
GGAACATTCA TCGTGGACAG CGTGGGAATTA CTTCTTATGG AGGAATAA      3468

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(2) INFORMATION FOR SEQ ID NO:2:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 3468 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: other nucleic acid
 - (A) DESCRIPTION: /desc = "Synthetic DNA"
- (iii) HYPOTHETICAL: NO
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION: 1..3468
 - (D) OTHER INFORMATION: /product= "Full-length pure maize optimized synthetic Bt"
 - /note= "Disclosed in Figure 3 as syn1T.mze"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

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TACGTGCAGG CCGCCAACCT GCACCTGAGC GTGCTGCGCG ACGTGAGCGT GTTCGGCCAG 540
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CCCGACAGCC GCGACTGGAT CCGCTACAAC CAGTTCCGCC GCGAGCTGAC CCTGACCGTG 720
CTGGACATCG TGAGCCTGTT CCCCAACTAC GACAGCCGCA CCTACCCCAT CCGCACCGTG 780
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GTGCTGGTGG TGCCCGAGTG GGAGGCCGAG GTGAGCCAGG AGGTGCGCGT GTGCCCCGGC	3000
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GTGTACCCCA ACAACACCGT GACCTGCAAC GACTACACCG CCACCCAGGA GGAGTACGAG	3180
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(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1947 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

- (A) DESCRIPTION: /desc = "Synthetic DNA"

(iii) HYPOTHETICAL: NO

(ix) FEATURE:
 (A) NAME/KEY: misc_feature
 (B) LOCATION: 1..1947
 (D) OTHER INFORMATION: /product= "Truncated synthetic
 maize optimized cryIA(b) gene"
 /note= "Disclosed in Figures 1, 2, 3, 4 and 5 as bssyn."

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

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(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 3468 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

- (A) DESCRIPTION: /desc = "Synthetic DNA"

(iii) HYPOTHETICAL: NO

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
 - (B) LOCATION: 1..3468
 - (D) OTHER INFORMATION: /product= "Full length synthetic maize optimized"
- /note= "Disclosed in Figure 3 as synful.mod. This sequence is identical to flsynbt.fin as disclosed in Figure 1."

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

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GAGTTCAACA	ACATCATCCC	CAGCAGCCAG	ATCACCCAGA	TCCCCCTGAC	CAAGAGCACC	1440
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ACCCTGCTGG	GCACCTTCGA	CGAGTGCTAC	CCCACCTACC	TGTACCAGAA	GATCGACGAG	2220
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GTGATCTTCA AGATCAAGAC CCAGGACGGC CACGCCCCGCC TGGGCAACCT GGAGTTCCTG 2520
 GAGGAGAAGC CCCTGGTGGG CGAGGCCCTG GCGCGCGTGA AGCGCGCCGA GAAGAAGTGG 2580
 CGCGACAAGC GCGAGAAGCT GGAGTGGGAG ACCAACATCG TGTACAAGGA GGCCAAGGAG 2640
 AGCGTGGACG CCCTGTTCGT GAACAGCCAG TACGACCGCC TGCAGGCCGA CACCAACATC 2700
 GCCATGATCC ACGCCGCCGA CAAGCGCGTG CACAGCATTC GCGAGGCCA CTGCCCCGAG 2760
 CTGAGCGTGA TCCCCGGCGT GAACGCCGCC ATCTTCGAGG AGCTGGAGGG CCGCATCTTC 2820
 ACCGCCTTCA GCCTGTACGA CGCCCGCAAC GTGATCAAGA ACGGCGACTT CAACAACGGC 2880
 CTGAGCTGCT GGAACGTGAA GGGCCACGTG GACGTGGAGG AGCAGAACAA CCACCGCAGC 2940
 GTGCTGGTGG TGCCCGAGTG GGAGGCCGAG GTGAGCCAGG AGGTGCGCGT GTGCCCCGGC 3000
 CGCGGCTACA TCCTGCGCGT GACCGCCTAC AAGGAGGGCT ACGGCGAGGG CTGCGTGACC 3060
 ATCCACGAGA TCGAGAACAA CACCGACGAG CTCAAGTTCA GCAACTGCGT GGAGGAGGAG 3120
 GTGTACCCCA ACAACACCGT GACCTGCAAC GACTACACCG CCACCCAGGA GGAGTACGAG 3180
 GGCACCTACA CCAGCCGCAA CCGCGGCTAC GACGGCGCCT ACGAGAGCAA CAGCAGCGTG 3240
 CCCGCCGACT ACGCCAGCGC CTACGAGGAG AAGGCCTACA CCGACGGCCG CCGCGACAAC 3300
 CCCTGCGAGA GCAACCGCGG CTACGGCGAC TACACCCCCC TGCCCGCCGG CTACGTGACC 3360
 AAGGAGCTGG AGTACTTCCC CGAGACCGAC AAGGTGTGGA TCGAGATCGG CGAGACCGAG 3420
 GGCACCTTCA TCGTGGACAG CGTGGAGCTG CTGCTGATGG AGGAGTAG 3468

(2) INFORMATION FOR SEQ ID NO:5:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1845 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

- (A) DESCRIPTION: /desc = "Synthetic DNA"

(iii) HYPOTHETICAL: NO

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION: 1..1845
- (D) OTHER INFORMATION: /note= "This is the synthetic Bt gene according to Perlak et al. as shown in Figures 4 and 5 as PMONBT."

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

ATGGACAACA ACCCAAACAT CAACGAATGC ATTCCATACA ACTGCTTGAG TAACCCAGAA 60

GTTGAAGTAC	TTGGTGGAGA	ACGCATTGAA	ACCGGTTACA	CTCCCATCGA	CATCTCCTTG	120
TCCTTGACAC	AGTTTCTGCT	CAGCGAGTTC	GTGCCAGGTG	CTGGGTTCGT	TCTCGGACTA	180
GTTGACATCA	TCTGGGGTAT	CTTTGGTCCA	TCTCAATGGG	ATGCATTCTT	GGTGCAAATT	240
GAGCAGTTGA	TCAACCAGAG	GATCGAAGAG	TTCGCCAGGA	ACCAGGCCAT	CTCTAGGTTG	300
GAAGGATTGA	GCAATCTCTA	CCAAATCTAT	GCAGAGAGCT	TCAGAGAGTG	GGAAGCCGAT	360
CCTACTAACC	CAGCTCTCCG	CGAGGAAATG	CGTATTCAAT	TCAACGACAT	GAACAGCGCC	420
TTGACCACAG	CTATCCCATT	GTTTCGCAGTC	CAGAACTACC	AAGTTCCTCT	CTTGTCCGTG	480
TACGTTCAAG	CAGCTAATCT	TCACCTCAGC	GTGCTTCGAG	ACGTTAGCGT	GTTTGGGCAA	540
AGGTGGGGAT	TCGATGCTGC	AACCATCAAT	AGCCGTTACA	ACGACCTTAC	TAGGCTGATT	600
GGAAACTACA	CCGACCACGC	TGTTTCGTTGG	TACAACACTG	GCTTGGAGCG	TGTCTGGGGT	660
CCTGATTCTA	GAGATTGGAT	TAGATACAAC	CAGTTCAGGA	GAGAATTGAC	CCTCACAGTT	720
TTGGACATTG	TGTCTCTCTT	CCCGAACTAT	GACTCCAGAA	CCTACCCTAT	CCGTACAGTG	780
TCCCAACTTA	CCAGAGAAAT	CTATACTAAC	CCAGTTCTTG	AGAACTTCGA	CGGTAGCTTC	840
CGTGGTTCTG	CCCAAGGTAT	CGAAGGCTCC	ATCAGGAGCC	CACACTTGAT	GGACATCTTG	900
AACAGCATAA	CTATCTACAG	CGATGCTCAC	AGAGGAGAGT	ATTACTGGTC	TGGACACCAG	960
ATCATGGCCT	CTCCAGTTGG	ATTCAGCGGG	CCCGAGTTTA	CCTTTCCTCT	CTATGGAAct	1020
ATGGGAAACG	CCGCTCCACA	ACAACGTATC	GTGCTCAAC	TAGGTCAGGG	TGTCTACAGA	1080
ACCTTGTCTT	CCACCTTGTA	CAGAAGACCC	TTCAATATCG	GTATCAACAA	CCAGCAACTT	1140
TCCGTTCTTG	ACGGAACAGA	GTTTCGCCTAT	GGAACCTCTT	CTAACTTGCC	ATCCGCTGTT	1200
TACAGAAAGA	GCGGAACCGT	TGATTCTCTG	GACGAAATCC	CACCACAGAA	CAACAATGTG	1260
CCACCCAGGC	AAGGATTCTC	CCACAGGTTG	AGCCACGTGT	CCATGTTCCG	TTCCGGATTG	1320
AGCAACAGTT	CCGTGAGCAT	CATCAGAGCT	CCTATGTTCT	CATGGATTCA	TCGTAGTGCT	1380
GAGTTCAACA	ATATCATTCC	TTCCTCTCAA	ATCACCCAAA	TCCCATTGAC	CAAGTCTACT	1440
AACCTTGGAT	CTGGAActTC	TGTCGTGAAA	GGACCAGGCT	TCACAGGAGG	TGATATTCTT	1500
AGAAGAACTT	CTCCTGGCCA	GATTAGCACC	CTCAGAGTTA	ACATCACTGC	ACCACTTTCT	1560
CAAAGATATC	GTGTCAGGAT	TCGTTACGCA	TCTACCACTA	ACTTGCAATT	CCACACCTCC	1620
ATCGACGGAA	GGCCTATCAA	TCAGGGTAAC	TTCTCCGCAA	CCATGTCAAG	CGGCAGCAAC	1680
TTGCAATCCG	GCAGCTTCAG	AACCGTCGGT	TTCActACTC	CTTTCAACTT	CTCTAACGGA	1740
TCAAGCGTTT	TCACCCTTAG	CGCTCATGTG	TTCAATTCTG	GCAATGAAGT	GTACATTGAC	1800
CGTATTGAGT	TTGTGCCTGC	CGAAGTTACC	TTCGAGGCTG	AGTAC		1845

(2) INFORMATION FOR SEQ ID NO:6:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 3624 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid
 (A) DESCRIPTION: /desc = "Synthetic DNA"

(iii) HYPOTHETICAL: NO

(ix) FEATURE:
 (A) NAME/KEY: CDS
 (B) LOCATION: 1..3621
 (D) OTHER INFORMATION: /product= "Full-length, maize
 optimized cryIB"
 /note= "Disclosed in Figure 6."

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

ATG GAC CTG CTG CCC GAC GCC CGC ATC GAG GAC AGC CTG TGC ATC GCC	48
Met Asp Leu Leu Pro Asp Ala Arg Ile Glu Asp Ser Leu Cys Ile Ala	
1 5 10 15	
GAG GGC AAC AAC ATC GAC CCC TTC GTG AGC GCC AGC ACC GTG CAG ACC	96
Glu Gly Asn Asn Ile Asp Pro Phe Val Ser Ala Ser Thr Val Gln Thr	
20 25 30	
GGC ATC AAC ATC GCC GGC CGC ATC CTG GGC GTG CTG GGC GTG CCC TTC	144
Gly Ile Asn Ile Ala Gly Arg Ile Leu Gly Val Leu Gly Val Pro Phe	
35 40 45	
GCC GGC CAG CTG GCC AGC TTC TAC AGC TTC CTG GTG GGC GAG CTG TGG	192
Ala Gly Gln Leu Ala Ser Phe Tyr Ser Phe Leu Val Gly Glu Leu Trp	
50 55 60	
CCC CGC GGC CGC GAC CAG TGG GAG ATC TTC CTG GAG CAC GTG GAG CAG	240
Pro Arg Gly Arg Asp Gln Trp Glu Ile Phe Leu Glu His Val Glu Gln	
65 70 75 80	
CTG ATC AAC CAG CAG ATC ACC GAG AAC GCC CGC AAC ACC GCC CTG GCC	288
Leu Ile Asn Gln Gln Ile Thr Glu Asn Ala Arg Asn Thr Ala Leu Ala	
85 90 95	
CGC CTG CAG GGC CTG GGC GAC AGC TTC CGC GCC TAC CAG CAG AGC CTG	336
Arg Leu Gln Gly Leu Gly Asp Ser Phe Arg Ala Tyr Gln Gln Ser Leu	
100 105 110	
GAG GAC TGG CTG GAG AAC CGC GAC GAC GCC CGC ACC CGC AGC GTG CTG	384
Glu Asp Trp Leu Glu Asn Arg Asp Asp Ala Arg Thr Arg Ser Val Leu	
115 120 125	
TAC ACC CAG TAC ATC GCC CTG GAG CTG GAC TTC CTG AAC GCC ATG CCC	432
Tyr Thr Gln Tyr Ile Ala Leu Glu Leu Asp Phe Leu Asn Ala Met Pro	
130 135 140	
CTG TTC GCC ATC CGC AAC CAG GAG GTG CCC CTG CTG ATG GTG TAC GCC	480
Leu Phe Ala Ile Arg Asn Gln Glu Val Pro Leu Leu Met Val Tyr Ala	

145					150					155					160	
CAG	GCC	GCC	AAC	CTG	CAC	CTG	CTG	CTG	CTG	CGC	GAC	GCC	AGC	CTG	TTC	528
Gln	Ala	Ala	Asn	Leu	His	Leu	Leu	Leu	Leu	Arg	Asp	Ala	Ser	Leu	Phe	
				165						170				175		
GGC	AGC	GAG	TTC	GGC	CTG	ACC	AGC	CAG	GAG	ATC	CAG	CGC	TAC	TAC	GAG	576
Gly	Ser	Glu	Phe	Gly	Leu	Thr	Ser	Gln	Glu	Ile	Gln	Arg	Tyr	Tyr	Glu	
			180					185					190			
CGC	CAG	GTG	GAG	CGC	ACC	CGC	GAC	TAC	AGC	GAC	TAC	TGC	GTG	GAG	TGG	624
Arg	Gln	Val	Glu	Arg	Thr	Arg	Asp	Tyr	Ser	Asp	Tyr	Cys	Val	Glu	Trp	
		195					200					205				
TAC	AAC	ACC	GGC	CTG	AAC	AGC	CTG	CGC	GGC	ACC	AAC	GCC	GCC	AGC	TGG	672
Tyr	Asn	Thr	Gly	Leu	Asn	Ser	Leu	Arg	Gly	Thr	Asn	Ala	Ala	Ser	Trp	
	210					215					220					
GTG	CGC	TAC	AAC	CAG	TTC	CGC	CGC	GAC	CTG	ACC	CTG	GGC	GTG	CTG	GAC	720
Val	Arg	Tyr	Asn	Gln	Phe	Arg	Arg	Asp	Leu	Thr	Leu	Gly	Val	Leu	Asp	
225				230				235							240	
CTG	GTG	GCC	CTG	TTC	CCC	AGC	TAC	GAC	ACC	CGC	ACC	TAC	CCC	ATC	AAC	768
Leu	Val	Ala	Leu	Phe	Pro	Ser	Tyr	Asp	Thr	Arg	Thr	Tyr	Pro	Ile	Asn	
				245				250						255		
ACC	AGC	GCC	CAG	CTG	ACC	CGC	GAG	GTG	TAC	ACC	GAC	GCC	ATC	GGC	GCC	816
Thr	Ser	Ala	Gln	Leu	Thr	Arg	Glu	Val	Tyr	Thr	Asp	Ala	Ile	Gly	Ala	
			260					265					270			
ACC	GGC	GTG	AAC	ATG	GCC	AGC	ATG	AAC	TGG	TAC	AAC	AAC	AAC	GCC	CCC	864
Thr	Gly	Val	Asn	Met	Ala	Ser	Met	Asn	Trp	Tyr	Asn	Asn	Asn	Ala	Pro	
		275					280					285				
AGC	TTC	AGC	GCC	ATC	GAG	GCC	GCC	GCC	ATC	CGC	AGC	CCC	CAC	CTG	CTG	912
Ser	Phe	Ser	Ala	Ile	Glu	Ala	Ala	Ala	Ile	Arg	Ser	Pro	His	Leu	Leu	
	290					295					300					
GAC	TTC	CTG	GAG	CAG	CTG	ACC	ATC	TTC	AGC	GCC	AGC	AGC	CGC	TGG	AGC	960
Asp	Phe	Leu	Glu	Gln	Leu	Thr	Ile	Phe	Ser	Ala	Ser	Ser	Arg	Trp	Ser	
305				310				315						320		
AAC	ACC	CGC	CAC	ATG	ACC	TAC	TGG	CGC	GGC	CAC	ACC	ATC	CAG	AGC	CGC	1008
Asn	Thr	Arg	His	Met	Thr	Tyr	Trp	Arg	Gly	His	Thr	Ile	Gln	Ser	Arg	
				325				330						335		
CCC	ATC	GGC	GGC	GGC	CTG	AAC	ACC	AGC	ACC	CAC	GGC	GCC	ACC	AAC	ACC	1056
Pro	Ile	Gly	Gly	Gly	Leu	Asn	Thr	Ser	Thr	His	Gly	Ala	Thr	Asn	Thr	
			340					345				350				
AGC	ATC	AAC	CCC	GTG	ACC	CTG	CGC	TTC	GCC	AGC	CGC	GAC	GTG	TAC	CGC	1104
Ser	Ile	Asn	Pro	Val	Thr	Leu	Arg	Phe	Ala	Ser	Arg	Asp	Val	Tyr	Arg	
		355					360					365				
ACC	GAG	AGC	TAC	GCC	GGC	GTG	CTG	CTG	TGG	GGC	ATC	TAC	CTG	GAG	CCC	1152
Thr	Glu	Ser	Tyr	Ala	Gly	Val	Leu	Leu	Trp	Gly	Ile	Tyr	Leu	Glu	Pro	
	370					375					380					
ATC	CAC	GGC	GTG	CCC	ACC	GTG	CGC	TTC	AAC	TTC	ACC	AAC	CCC	CAG	AAC	1200
Ile	His	Gly	Val	Pro	Thr	Val	Arg	Phe	Asn	Phe	Thr	Asn	Pro	Gln	Asn	
385				390					395					400		

ATC	AGC	GAC	CGC	GGC	ACC	GCC	AAC	TAC	AGC	CAG	CCC	TAC	GAG	AGC	CCC	1248
Ile	Ser	Asp	Arg	Gly	Thr	Ala	Asn	Tyr	Ser	Gln	Pro	Tyr	Glu	Ser	Pro	
				405					410					415		
GGC	CTG	CAG	CTG	AAG	GAC	AGC	GAG	ACC	GAG	CTG	CCC	CCC	GAG	ACC	ACC	1296
Gly	Leu	Gln	Leu	Lys	Asp	Ser	Glu	Thr	Glu	Leu	Pro	Pro	Glu	Thr	Thr	
			420					425					430			
GAG	CGC	CCC	AAC	TAC	GAG	AGC	TAC	AGC	CAC	CGC	CTG	AGC	CAC	ATC	GGC	1344
Glu	Arg	Pro	Asn	Tyr	Glu	Ser	Tyr	Ser	His	Arg	Leu	Ser	His	Ile	Gly	
		435					440					445				
ATC	ATC	CTG	CAG	AGC	CGC	GTG	AAC	GTG	CCC	GTG	TAC	AGC	TGG	ACC	CAC	1392
Ile	Ile	Leu	Gln	Ser	Arg	Val	Asn	Val	Pro	Val	Tyr	Ser	Trp	Thr	His	
	450					455					460					
CGC	AGC	GCC	GAC	CGC	ACC	AAC	ACC	ATC	GGC	CCC	AAC	CGC	ATC	ACC	CAG	1440
Arg	Ser	Ala	Asp	Arg	Thr	Asn	Thr	Ile	Gly	Pro	Asn	Arg	Ile	Thr	Gln	
465					470				475						480	
ATC	CCC	ATG	GTG	AAG	GCC	AGC	GAG	CTG	CCC	CAG	GGC	ACC	ACC	GTG	GTG	1488
Ile	Pro	Met	Val	Lys	Ala	Ser	Glu	Leu	Pro	Gln	Gly	Thr	Thr	Val	Val	
				485					490					495		
CGC	GGC	CCC	GGC	TTC	ACC	GGC	GGC	GAC	ATC	CTG	CGC	CGC	ACC	AAC	ACC	1536
Arg	Gly	Pro	Gly	Phe	Thr	Gly	Gly	Asp	Ile	Leu	Arg	Arg	Thr	Asn	Thr	
			500					505					510			
GGC	GGC	TTC	GGC	CCC	ATC	CGC	GTG	ACC	GTG	AAC	GGC	CCC	CTG	ACC	CAG	1584
Gly	Gly	Phe	Gly	Pro	Ile	Arg	Val	Thr	Val	Asn	Gly	Pro	Leu	Thr	Gln	
		515					520					525				
CGC	TAC	CGC	ATC	GGC	TTC	CGC	TAC	GCC	AGC	ACC	GTG	GAC	TTC	GAC	TTC	1632
Arg	Tyr	Arg	Ile	Gly	Phe	Arg	Tyr	Ala	Ser	Thr	Val	Asp	Phe	Asp	Phe	
	530					535					540					
TTC	GTG	AGC	CGC	GGC	GGC	ACC	ACC	GTG	AAC	AAC	TTC	CGC	TTC	CTG	CGC	1680
Phe	Val	Ser	Arg	Gly	Gly	Thr	Thr	Val	Asn	Asn	Phe	Arg	Phe	Leu	Arg	
545					550				555						560	
ACC	ATG	AAC	AGC	GGC	GAC	GAG	CTG	AAG	TAC	GGC	AAC	TTC	GTG	CGC	CGC	1728
Thr	Met	Asn	Ser	Gly	Asp	Glu	Leu	Lys	Tyr	Gly	Asn	Phe	Val	Arg	Arg	
				565					570					575		
GCC	TTC	ACC	ACC	CCC	TTC	ACC	TTC	ACC	CAG	ATC	CAG	GAC	ATC	ATC	CGC	1776
Ala	Phe	Thr	Thr	Pro	Phe	Thr	Phe	Thr	Gln	Ile	Gln	Asp	Ile	Ile	Arg	
			580					585					590			
ACC	AGC	ATC	CAG	GGC	CTG	AGC	GGC	AAC	GGC	GAG	GTG	TAC	ATC	GAC	AAG	1824
Thr	Ser	Ile	Gln	Gly	Leu	Ser	Gly	Asn	Gly	Glu	Val	Tyr	Ile	Asp	Lys	
		595					600					605				
ATC	GAG	ATC	ATC	CCC	GTG	ACC	GCC	ACC	TTC	GAG	GCC	GAG	TAC	GAC	CTG	1872
Ile	Glu	Ile	Ile	Pro	Val	Thr	Ala	Thr	Phe	Glu	Ala	Glu	Tyr	Asp	Leu	
	610					615					620					
GAG	CGC	GCC	CAG	GAG	GCC	GTG	AAC	GCC	CTG	TTC	ACC	AAC	ACC	AAC	CCC	1920
Glu	Arg	Ala	Gln	Glu	Ala	Val	Asn	Ala	Leu	Phe	Thr	Asn	Thr	Asn	Pro	
625					630				635						640	

CGC CGC CTG AAG ACC GAC GTG ACC GAC TAC CAC ATC GAC CAG GTG AGC Arg Arg Leu Lys Thr Asp Val Thr Asp Tyr His Ile Asp Gln Val Ser 645 650 655	1963
AAC CTG GTG GCC TGC CTG AGC GAC GAG TTC TGC CTG GAC GAG AAG CGC Asn Leu Val Ala Cys Leu Ser Asp Glu Phe Cys Leu Asp Glu Lys Arg 660 665 670	2015
GAG CTG CTG GAG AAG GTG AAG TAC GCC AAG CGC CTG AGC GAC GAG CGC Glu Leu Leu Glu Lys Val Lys Tyr Ala Lys Arg Leu Ser Asp Glu Arg 675 680 685	2064
AAC CTG CTG CAG GAC CCC AAC TTC ACC AGC ATC AAC AAG CAG CCC GAC Asn Leu Leu Gln Asp Pro Asn Phe Thr Ser Ile Asn Lys Gln Pro Asp 690 695 700	2112
TTC ATC AGC ACC AAC GAG CAG AGC AAC TTC ACC AGC ATC CAC GAG CAG Phe Ile Ser Thr Asn Glu Gln Ser Asn Phe Thr Ser Ile His Glu Gln 705 710 715 720	2163
AGC GAG CAC GGC TGG TGG GGC AGC GAG AAC ATC ACC ATC CAG GAG GGC Ser Glu His Gly Trp Trp Gly Ser Glu Asn Ile Thr Ile Gln Glu Gly 725 730 735	2208
AAC GAC GTG TTC AAG GAG AAC TAC GTG ACC CTG CCC GGC ACC TTC AAC Asn Asp Val Phe Lys Glu Asn Tyr Val Thr Leu Pro Gly Thr Phe Asn 740 745 750	2256
GAG TGC TAC CCC ACC TAC CTG TAC CAG AAG ATC GGC GAG AGC GAG CTG Glu Cys Tyr Pro Thr Tyr Leu Tyr Gln Lys Ile Gly Glu Ser Glu Leu 755 760 765	2304
AAG GCC TAC ACC CGC TAC CAG CTG CGC GGC TAC ATC GAG GAC AGC CAG Lys Ala Tyr Thr Arg Tyr Gln Leu Arg Gly Tyr Ile Glu Asp Ser Gln 770 775 780	2352
GAC CTG GAG ATC TAC CTG ATC CGC TAC AAC GCC AAG CAC GAG ACC CTG Asp Leu Glu Ile Tyr Leu Ile Arg Tyr Asn Ala Lys His Glu Thr Leu 785 790 795 800	2400
GAC GTG CCC GGC ACC GAG AGC CTG TGG CCC CTG AGC GTG GAG AGC CCC Asp Val Pro Gly Thr Glu Ser Leu Trp Pro Leu Ser Val Glu Ser Pro 805 810 815	2448
ATC GGC CGC TGC GGC GAG CCC AAC CGC TGC GCC CCC CAC TTC GAG TGG Ile Gly Arg Cys Gly Glu Pro Asn Arg Cys Ala Pro His Phe Glu Trp 820 825 830	2496
AAC CCC GAC CTG GAC TGC AGC TGC CGC GAC GGC GAG AAG TGC GCC CAC Asn Pro Asp Leu Asp Cys Ser Cys Arg Asp Gly Glu Lys Cys Ala His 835 840 845	2544
CAC AGC CAC CAC TTC AGC CTG GAC ATC GAC GTG GGC TGC ACC GAC CTG His Ser His His Phe Ser Leu Asp Ile Asp Val Gly Cys Thr Asp Leu 850 855 860	2592
CAC GAG AAC CTG GGC GTG TGG GTG GTG TTC AAG ATC AAG ACC CAG GAG His Glu Asn Leu Gly Val Trp Val Val Phe Lys Ile Lys Thr Gln Glu 865 870 875 880	2640
GGC CAC GCC CGC CTG GGC AAC CTG GAG TTC ATC GAG GAG AAG CCC CTG	2688

Gly His Ala Arg Leu Gly Asn Leu Glu Phe Ile Glu Glu Lys Pro Leu	
885 890 895	
CTG GGC GAG GCC CTG AGC CGC GTG AAG CGC GCC GAG AAG AAG TGG CGC	2736
Leu Gly Glu Ala Leu Ser Arg Val Lys Arg Ala Glu Lys Lys Trp Arg	
900 905 910	
GAC AAG CGC GAG AAG CTG CAG CTG GAG ACC AAG CGC GTG TAC ACC GAG	2784
Asp Lys Arg Glu Lys Leu Gln Leu Glu Thr Lys Arg Val Tyr Thr Glu	
915 920 925	
GCC AAG GAG GCC GTG GAC GCC CTG TTC GTG GAC AGC CAG TAC GAC CGC	2832
Ala Lys Glu Ala Val Asp Ala Leu Phe Val Asp Ser Gln Tyr Asp Arg	
930 935 940	
CTG CAG GCC GAC ACC AAC ATC GGC ATG ATC CAC GCC GCC GAC AAG CTG	2880
Leu Gln Ala Asp Thr Asn Ile Gly Met Ile His Ala Ala Asp Lys Leu	
945 950 955 960	
GTG CAC CGC ATC CGC GAG GCC TAC CTG AGC GAG CTG CCC GTG ATC CCC	2928
Val His Arg Ile Arg Glu Ala Tyr Leu Ser Glu Leu Pro Val Ile Pro	
965 970 975	
GGC GTG AAC GCC GAG ATC TTC GAG GAG CTG GAG GGC CAC ATC ATC ACC	2976
Gly Val Asn Ala Glu Ile Phe Glu Glu Leu Glu Gly His Ile Ile Thr	
980 985 990	
GCC ATC AGC CTG TAC GAC GCC CGC AAC GTG GTG AAG AAC GGC GAC TTC	3024
Ala Ile Ser Leu Tyr Asp Ala Arg Asn Val Val Lys Asn Gly Asp Phe	
995 1000 1005	
AAC AAC GGC CTG ACC TGC TGG AAC GTG AAG GGC CAC GTG GAC GTG CAG	3072
Asn Asn Gly Leu Thr Cys Trp Asn Val Lys Gly His Val Asp Val Gln	
1010 1015 1020	
CAG AGC CAC CAC CGC AGC GAC CTG GTG ATC CCC GAG TGG GAG GCC GAG	3120
Gln Ser His His Arg Ser Asp Leu Val Ile Pro Glu Trp Glu Ala Glu	
1025 1030 1035 1040	
GTG AGC CAG GCC GTG CGC GTG TGC CCC GGC TGC GGC TAC ATC CTG CGC	3168
Val Ser Gln Ala Val Arg Val Cys Pro Gly Cys Gly Tyr Ile Leu Arg	
1045 1050 1055	
GTG ACC GCC TAC AAG GAG GGC TAC GGC GAG GGC TGC GTG ACC ATC CAC	3216
Val Thr Ala Tyr Lys Glu Gly Tyr Gly Glu Gly Cys Val Thr Ile His	
1060 1065 1070	
GAG ATC GAG AAC AAC ACC GAC GAG CTG AAG TTC AAG AAC CGC GAG GAG	3264
Glu Ile Glu Asn Asn Thr Asp Glu Leu Lys Phe Lys Asn Arg Glu Glu	
1075 1080 1085	
GAG GAG GTG TAC CCC ACC GAC ACC GGC ACC TGC AAC GAC TAC ACC GCC	3312
Glu Glu Val Tyr Pro Thr Asp Thr Gly Thr Cys Asn Asp Tyr Thr Ala	
1090 1095 1100	
CAC CAG GGC ACC GCC GGC TGC GCC GAC GCC TGC AAC AGC CGC AAC GCC	3360
His Gln Gly Thr Ala Gly Cys Ala Asp Ala Cys Asn Ser Arg Asn Ala	
1105 1110 1115 1120	
GGC TAC GAG GAC GCC TAC GAG GTG GAC ACC ACC GCC AGC GTG AAC TAC	3408
Gly Tyr Glu Asp Ala Tyr Glu Val Asp Thr Thr Ala Ser Val Asn Tyr	

	1125	1130	1135	
AAG CCC ACC TAC GAG GAG GAG ACC TAC ACC GAC GTG CGC CGC GAC AAC				3456
Lys Pro Thr Tyr Glu Glu Glu Thr Tyr Thr Asp Val Arg Arg Asp Asn				
	1140	1145	1150	
CAC TGC GAG TAC GAC CGC GGC TAC GTG AAC TAC CCC CCC GTG CCC GCC				3504
His Cys Glu Tyr Asp Arg Gly Tyr Val Asn Tyr Pro Pro Val Pro Ala				
	1155	1160	1165	
GGC TAC GTG ACC AAG GAG CTG GAG TAC TTC CCC GAG ACC GAC ACC GTG				3552
Gly Tyr Val Thr Lys Glu Leu Glu Tyr Phe Pro Glu Thr Asp Thr Val				
	1170	1175	1180	
TGG ATC GAG ATC GGC GAG ACC GAG GGC AAG TTC ATC GTG GAC AGC GTG				3600
Trp Ile Glu Ile Gly Glu Thr Glu Gly Lys Phe Ile Val Asp Ser Val				
	1185	1190	1195	1200
GAG CTG CTG CTG ATG GAG GAG TAG				3624
Glu Leu Leu Leu Met Glu Glu				
	1205			

(2) INFORMATION FOR SEQ ID NO:7:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1207 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

Met	Asp	Leu	Leu	Pro	Asp	Ala	Arg	Ile	Glu	Asp	Ser	Leu	Cys	Ile	Ala
1				5					10					15	
Glu	Gly	Asn	Asn	Ile	Asp	Pro	Phe	Val	Ser	Ala	Ser	Thr	Val	Gln	Thr
		20						25					30		
Gly	Ile	Asn	Ile	Ala	Gly	Arg	Ile	Leu	Gly	Val	Leu	Gly	Val	Pro	Phe
		35					40					45			
Ala	Gly	Gln	Leu	Ala	Ser	Phe	Tyr	Ser	Phe	Leu	Val	Gly	Glu	Leu	Trp
	50					55					60				
Pro	Arg	Gly	Arg	Asp	Gln	Trp	Glu	Ile	Phe	Leu	Glu	His	Val	Glu	Gln
	65				70				75					80	
Leu	Ile	Asn	Gln	Gln	Ile	Thr	Glu	Asn	Ala	Arg	Asn	Thr	Ala	Leu	Ala
			85					90						95	
Arg	Leu	Gln	Gly	Leu	Gly	Asp	Ser	Phe	Arg	Ala	Tyr	Gln	Gln	Ser	Leu
		100						105				110			
Glu	Asp	Trp	Leu	Glu	Asn	Arg	Asp	Asp	Ala	Arg	Thr	Arg	Ser	Val	Leu
	115						120				125				
Tyr	Thr	Gln	Tyr	Ile	Ala	Leu	Glu	Leu	Asp	Phe	Leu	Asn	Ala	Met	Pro
	130					135					140				

Leu Phe Ala Ile Arg Asn Gln Glu Val Pro Leu Leu Met Val Tyr Ala
 145 150 155 160
 Gln Ala Ala Asn Leu His Leu Leu Leu Leu Arg Asp Ala Ser Leu Phe
 165 170 175
 Gly Ser Glu Phe Gly Leu Thr Ser Gln Glu Ile Gln Arg Tyr Tyr Glu
 180 185 190
 Arg Gln Val Glu Arg Thr Arg Asp Tyr Ser Asp Tyr Cys Val Glu Trp
 195 200 205
 Tyr Asn Thr Gly Leu Asn Ser Leu Arg Gly Thr Asn Ala Ala Ser Trp
 210 215 220
 Val Arg Tyr Asn Gln Phe Arg Arg Asp Leu Thr Leu Gly Val Leu Asp
 225 230 235 240
 Leu Val Ala Leu Phe Pro Ser Tyr Asp Thr Arg Thr Tyr Pro Ile Asn
 245 250 255
 Thr Ser Ala Gln Leu Thr Arg Glu Val Tyr Thr Asp Ala Ile Gly Ala
 260 265 270
 Thr Gly Val Asn Met Ala Ser Met Asn Trp Tyr Asn Asn Asn Ala Pro
 275 280 285
 Ser Phe Ser Ala Ile Glu Ala Ala Ala Ile Arg Ser Pro His Leu Leu
 290 295 300
 Asp Phe Leu Glu Gln Leu Thr Ile Phe Ser Ala Ser Ser Arg Trp Ser
 305 310 315 320
 Asn Thr Arg His Met Thr Tyr Trp Arg Gly His Thr Ile Gln Ser Arg
 325 330 335
 Pro Ile Gly Gly Gly Leu Asn Thr Ser Thr His Gly Ala Thr Asn Thr
 340 345 350
 Ser Ile Asn Pro Val Thr Leu Arg Phe Ala Ser Arg Asp Val Tyr Arg
 355 360 365
 Thr Glu Ser Tyr Ala Gly Val Leu Leu Trp Gly Ile Tyr Leu Glu Pro
 370 375 380
 Ile His Gly Val Pro Thr Val Arg Phe Asn Phe Thr Asn Pro Gln Asn
 385 390 395 400
 Ile Ser Asp Arg Gly Thr Ala Asn Tyr Ser Gln Pro Tyr Glu Ser Pro
 405 410 415
 Gly Leu Gln Leu Lys Asp Ser Glu Thr Glu Leu Pro Pro Glu Thr Thr
 420 425 430
 Glu Arg Pro Asn Tyr Glu Ser Tyr Ser His Arg Leu Ser His Ile Gly
 435 440 445
 Ile Ile Leu Gln Ser Arg Val Asn Val Pro Val Tyr Ser Trp Thr His
 450 455 460
 Arg Ser Ala Asp Arg Thr Asn Thr Ile Gly Pro Asn Arg Ile Thr Gln

465		470		475		480
Ile Pro Met Val	Lys Ala Ser Glu Leu	Pro Gln Gly Thr Thr	Val Val			
	485	490	495			
Arg Gly Pro Gly	Phe Thr Gly Gly	Asp Ile Leu Arg Arg	Thr Asn Thr			
	500	505	510			
Gly Gly Phe Gly	Pro Ile Arg Val	Thr Val Asn Gly	Pro Leu Thr Gln			
	515	520	525			
Arg Tyr Arg Ile	Gly Phe Arg Tyr	Ala Ser Thr Val	Asp Phe Asp Phe			
	530	535	540			
Phe Val Ser Arg	Gly Gly Thr Thr	Val Asn Asn Phe	Arg Phe Leu Arg			
	545	550	555			560
Thr Met Asn Ser	Gly Asp Glu Leu	Lys Tyr Gly Asn	Phe Val Arg Arg			
	565	570	575			
Ala Phe Thr Thr	Pro Phe Thr Phe	Thr Gln Ile Gln	Asp Ile Ile Arg			
	580	585	590			
Thr Ser Ile Gln	Gly Leu Ser Gly	Asn Gly Glu Val	Tyr Ile Asp Lys			
	595	600	605			
Ile Glu Ile Ile	Pro Val Thr Ala	Thr Phe Glu Ala	Glu Tyr Asp Leu			
	610	615	620			
Glu Arg Ala Gln	Glu Ala Val Asn	Ala Leu Phe Thr	Asn Thr Asn Pro			
	625	630	635			640
Arg Arg Leu Lys	Thr Asp Val Thr	Asp Tyr His Ile	Asp Gln Val Ser			
	645	650	655			
Asn Leu Val Ala	Cys Leu Ser Asp	Glu Phe Cys Leu	Asp Glu Lys Arg			
	660	665	670			
Glu Leu Leu Glu	Lys Val Lys Tyr	Ala Lys Arg Leu	Ser Asp Glu Arg			
	675	680	685			
Asn Leu Leu Gln	Asp Pro Asn Phe	Thr Ser Ile Asn	Lys Gln Pro Asp			
	690	695	700			
Phe Ile Ser Thr	Asn Glu Gln Ser	Asn Phe Thr Ser	Ile His Glu Gln			
	705	710	715			720
Ser Glu His Gly	Trp Trp Gly Ser	Glu Asn Ile Thr	Ile Gln Glu Gly			
	725	730	735			
Asn Asp Val Phe	Lys Glu Asn Tyr	Val Thr Leu Pro	Gly Thr Phe Asn			
	740	745	750			
Glu Cys Tyr Pro	Thr Tyr Leu Tyr	Gln Lys Ile Gly	Glu Ser Glu Leu			
	755	760	765			
Lys Ala Tyr Thr	Arg Tyr Gln Leu	Arg Gly Tyr Ile	Glu Asp Ser Gln			
	770	775	780			
Asp Leu Glu Ile	Tyr Leu Ile Arg	Tyr Asn Ala Lys	His Glu Thr Leu			
	785	790	795			800

Asp	Val	Pro	Gly	Thr	Glu	Ser	Leu	Trp	Pro	Leu	Ser	Val	Glu	Ser	Pro	
				805					810					815		
Ile	Gly	Arg	Cys	Gly	Glu	Pro	Asn	Arg	Cys	Ala	Pro	His	Phe	Glu	Trp	
			820					825					830			
Asn	Pro	Asp	Leu	Asp	Cys	Ser	Cys	Arg	Asp	Gly	Glu	Lys	Cys	Ala	His	
		835					840					845				
His	Ser	His	His	Phe	Ser	Leu	Asp	Ile	Asp	Val	Gly	Cys	Thr	Asp	Leu	
	850					855					860					
His	Glu	Asn	Leu	Gly	Val	Trp	Val	Val	Phe	Lys	Ile	Lys	Thr	Gln	Glu	
865					870					875					880	
Gly	His	Ala	Arg	Leu	Gly	Asn	Leu	Glu	Phe	Ile	Glu	Glu	Lys	Pro	Leu	
				885					890					895		
Leu	Gly	Glu	Ala	Leu	Ser	Arg	Val	Lys	Arg	Ala	Glu	Lys	Lys	Trp	Arg	
			900					905					910			
Asp	Lys	Arg	Glu	Lys	Leu	Gln	Leu	Glu	Thr	Lys	Arg	Val	Tyr	Thr	Glu	
		915					920						925			
Ala	Lys	Glu	Ala	Val	Asp	Ala	Leu	Phe	Val	Asp	Ser	Gln	Tyr	Asp	Arg	
	930					935					940					
Leu	Gln	Ala	Asp	Thr	Asn	Ile	Gly	Met	Ile	His	Ala	Ala	Asp	Lys	Leu	
945					950					955					960	
Val	His	Arg	Ile	Arg	Glu	Ala	Tyr	Leu	Ser	Glu	Leu	Pro	Val	Ile	Pro	
				965					970					975		
Gly	Val	Asn	Ala	Glu	Ile	Phe	Glu	Glu	Leu	Glu	Gly	His	Ile	Ile	Thr	
			980					985					990			
Ala	Ile	Ser	Leu	Tyr	Asp	Ala	Arg	Asn	Val	Val	Lys	Asn	Gly	Asp	Phe	
		995					1000					1005				
Asn	Asn	Gly	Leu	Thr	Cys	Trp	Asn	Val	Lys	Gly	His	Val	Asp	Val	Gln	
	1010					1015					1020					
Gln	Ser	His	His	Arg	Ser	Asp	Leu	Val	Ile	Pro	Glu	Trp	Glu	Ala	Glu	
1025					1030					1035					1040	
Val	Ser	Gln	Ala	Val	Arg	Val	Cys	Pro	Gly	Cys	Gly	Tyr	Ile	Leu	Arg	
				1045					1050					1055		
Val	Thr	Ala	Tyr	Lys	Glu	Gly	Tyr	Gly	Glu	Gly	Cys	Val	Thr	Ile	His	
			1060					1065					1070			
Glu	Ile	Glu	Asn	Asn	Thr	Asp	Glu	Leu	Lys	Phe	Lys	Asn	Arg	Glu	Glu	
		1075					1080					1085				
Glu	Glu	Val	Tyr	Pro	Thr	Asp	Thr	Gly	Thr	Cys	Asn	Asp	Tyr	Thr	Ala	
		1090					1095					1100				
His	Gln	Gly	Thr	Ala	Gly	Cys	Ala	Asp	Ala	Cys	Asn	Ser	Arg	Asn	Ala	
1105					1110					1115					1120	

Gly Tyr Glu Asp Ala Tyr Glu Val Asp Thr Thr Ala Ser Val Asn Tyr
1125 1130 1135

Lys Pro Thr Tyr Glu Glu Glu Thr Tyr Thr Asp Val Arg Arg Asp Asn
1140 1145 1150

His Cys Glu Tyr Asp Arg Gly Tyr Val Asn Tyr Pro Pro Val Pro Ala
1155 1160 1165

Gly Tyr Val Thr Lys Glu Leu Glu Tyr Phe Pro Glu Thr Asp Thr Val
1170 1175 1180

Trp Ile Glu Ile Gly Glu Thr Glu Gly Lys Phe Ile Val Asp Ser Val
1185 1190 1195 1200

Glu Leu Leu Leu Met Glu Glu
1205

(2) INFORMATION FOR SEQ ID NO:8:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 3468 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: other nucleic acid
(A) DESCRIPTION: /desc = "Synthetic DNA"
- (iii) HYPOTHETICAL: NO
- (ix) FEATURE:
(A) NAME/KEY: CDS
(B) LOCATION: 1..3465
(D) OTHER INFORMATION: /product= "Full-length, hybrid,
partially maize optimized cryIA(b)"
/note= "Disclosed in Figure 7 as contained in pCIB4434."

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

ATG GAC AAC AAC CCC AAC ATC AAC GAG TGC ATC CCC TAC AAC TGC CTG	48
Met Asp Asn Asn Pro Asn Ile Asn Glu Cys Ile Pro Tyr Asn Cys Leu	
1210 1215 1220	
AGC AAC CCC GAG GTG GAG GTG CTG GGC GGC GAG CGC ATC GAG ACC GGC	96
Ser Asn Pro Glu Val Glu Val Leu Gly Gly Glu Arg Ile Glu Thr Gly	
1225 1230 1235	
TAC ACC CCC ATC GAC ATC AGC CTG AGC CTG ACC CAG TTC CTG CTG AGC	144
Tyr Thr Pro Ile Asp Ile Ser Leu Ser Leu Thr Gln Phe Leu Leu Ser	
1240 1245 1250 1255	
GAG TTC GTG CCC GGC GCC GGC TTC GTG CTG GGC CTG GTG GAC ATC ATC	192
Glu Phe Val Pro Gly Ala Gly Phe Val Leu Gly Leu Val Asp Ile Ile	
1260 1265 1270	
TGG GGC ATC TTC GGC CCC AGC CAG TGG GAC GCC TTC CTG GTG CAG ATC	240
Trp Gly Ile Phe Gly Pro Ser Gln Trp Asp Ala Phe Leu Val Gln Ile	
1275 1280 1285	

GAG CAG CTG ATC AAC CAG CGC ATC GAG GAG TTC GCC CGC AAC CAG GCC Glu Gln Leu Ile Asn Gln Arg Ile Glu Glu Phe Ala Arg Asn Gln Ala 1290 1295 1300	288
ATC AGC CGC CTG GAG GGC CTG AGC AAC CTG TAC CAA ATC TAC GCC GAG Ile Ser Arg Leu Glu Gly Leu Ser Asn Leu Tyr Gln Ile Tyr Ala Glu 1305 1310 1315	336
AGC TTC CGC GAG TGG GAG GCC GAC CCC ACC AAC CCC GCC CTG CGC GAG Ser Phe Arg Glu Trp Glu Ala Asp Pro Thr Asn Pro Ala Leu Arg Glu 1320 1325 1330 1335	384
GAG ATG CGC ATC CAG TTC AAC GAC ATG AAC AGC GCC CTG ACC ACC GCC Glu Met Arg Ile Gln Phe Asn Asp Met Asn Ser Ala Leu Thr Thr Ala 1340 1345 1350	432
ATC CCC CTG TTC GCC GTG CAG AAC TAC CAG GTG CCC CTG CTG AGC GTG Ile Pro Leu Phe Ala Val Gln Asn Tyr Gln Val Pro Leu Leu Ser Val 1355 1360 1365	480
TAC GTG CAG GCC GCC AAC CTG CAC CTG AGC GTG CTG CGC GAC GTC AGC Tyr Val Gln Ala Ala Asn Leu His Leu Ser Val Leu Arg Asp Val Ser 1370 1375 1380	528
GTG TTC GGC CAG CGC TGG GGC TTC GAC GCC GCC ACC ATC AAC AGC CGC Val Phe Gly Gln Arg Trp Gly Phe Asp Ala Ala Thr Ile Asn Ser Arg 1385 1390 1395	576
TAC AAC GAC CTG ACC CGC CTG ATC GGC AAC TAC ACC GAC CAC GCC GTG Tyr Asn Asp Leu Thr Arg Leu Ile Gly Asn Tyr Thr Asp His Ala Val 1400 1405 1410 1415	624
CGC TGG TAC AAC ACC GGC CTG GAG CGC GTG TGG GGT CCC GAC AGC CGC Arg Trp Tyr Asn Thr Gly Leu Glu Arg Val Trp Gly Pro Asp Ser Arg 1420 1425 1430	672
GAC TGG ATC AGG TAC AAC CAG TTC CGC CGC GAG CTG ACC CTG ACC GTG Asp Trp Ile Arg Tyr Asn Gln Phe Arg Arg Glu Leu Thr Leu Thr Val 1435 1440 1445	720
CTG GAC ATC GTG AGC CTG TTC CCC AAC TAC GAC AGC CGC ACC TAC CCC Leu Asp Ile Val Ser Leu Phe Pro Asn Tyr Asp Ser Arg Thr Tyr Pro 1450 1455 1460	768
ATC CGC ACC GTG AGC CAG CTG ACC CGC GAG ATT TAC ACC AAC CCC GTG Ile Arg Thr Val Ser Gln Leu Thr Arg Glu Ile Tyr Thr Asn Pro Val 1465 1470 1475	816
CTG GAG AAC TTC GAC GGC AGC TTC CGC GGC AGC GCC CAG GGC ATC GAG Leu Glu Asn Phe Asp Gly Ser Phe Arg Gly Ser Ala Gln Gly Ile Glu 1480 1485 1490 1495	864
GGC AGC ATC CGC AGC CCC CAC CTG ATG GAC ATC CTG AAC AGC ATC ACC Gly Ser Ile Arg Ser Pro His Leu Met Asp Ile Leu Asn Ser Ile Thr 1500 1505 1510	912
ATC TAC ACC GAC GCC CAC CGC GGC GAG TAC TAC TGG AGC GGC CAC CAG Ile Tyr Thr Asp Ala His Arg Gly Glu Tyr Tyr Trp Ser Gly His Gln 1515 1520 1525	960

ATC	ATG	GCC	AGC	CCC	GTC	GGC	TTC	AGC	GGC	CCC	GAG	TTC	ACC	TTC	CCC	1008
Ile	Met	Ala	Ser	Pro	Val	Gly	Phe	Ser	Gly	Pro	Glu	Phe	Thr	Phe	Pro	
		1530					1535					1540				
CTG	TAC	GGC	ACC	ATG	GGC	AAC	GCT	GCA	CCT	CAG	CAG	CGC	ATC	GTG	GCA	1056
Leu	Tyr	Gly	Thr	Met	Gly	Asn	Ala	Ala	Pro	Gln	Gln	Arg	Ile	Val	Ala	
		1545				1550					1555					
CAG	CTG	GGC	CAG	GGA	GTG	TAC	CGC	ACC	CTG	AGC	AGC	ACC	CTG	TAC	CGT	1104
Gln	Leu	Gly	Gln	Gly	Val	Tyr	Arg	Thr	Leu	Ser	Ser	Thr	Leu	Tyr	Arg	
		1560			1565					1570					1575	
CGA	CCT	TTC	AAC	ATC	GGC	ATC	AAC	AAC	CAG	CAG	CTG	AGC	GTG	CTG	GAC	1152
Arg	Pro	Phe	Asn	Ile	Gly	Ile	Asn	Asn	Gln	Gln	Leu	Ser	Val	Leu	Asp	
				1580					1585						1590	
GGC	ACC	GAG	TTC	GCC	TAC	GGC	ACC	AGC	AGC	AAC	CTG	CCC	AGC	GCC	GTG	1200
Gly	Thr	Glu	Phe	Ala	Tyr	Gly	Thr	Ser	Ser	Asn	Leu	Pro	Ser	Ala	Val	
			1595					1600					1605			
TAC	CGC	AAG	AGC	GGC	ACC	GTG	GAC	AGC	CTG	GAC	GAG	ATC	CCC	CCT	CAG	1248
Tyr	Arg	Lys	Ser	Gly	Thr	Val	Asp	Ser	Leu	Asp	Glu	Ile	Pro	Pro	Gln	
		1610					1615					1620				
AAC	AAC	AAC	GTG	CCA	CCT	CGA	CAG	GGC	TTC	AGC	CAC	CGT	CTG	AGC	CAC	1296
Asn	Asn	Asn	Val	Pro	Pro	Arg	Gln	Gly	Phe	Ser	His	Arg	Leu	Ser	His	
		1625				1630					1635					
GTG	AGC	ATG	TTC	CGC	AGT	GGC	TTC	AGC	AAC	AGC	AGC	GTG	AGC	ATC	ATC	1344
Val	Ser	Met	Phe	Arg	Ser	Gly	Phe	Ser	Asn	Ser	Ser	Val	Ser	Ile	Ile	
		1640			1645				1650						1655	
CGT	GCA	CCT	ATG	TTC	AGC	TGG	ATT	CAC	CGC	AGT	GCC	GAG	TTC	AAC	AAC	1392
Arg	Ala	Pro	Met	Phe	Ser	Trp	Ile	His	Arg	Ser	Ala	Glu	Phe	Asn	Asn	
				1660					1665						1670	
ATC	ATC	CCC	AGC	AGC	CAG	ATC	ACC	CAG	ATC	CCC	CTG	ACC	AAG	AGC	ACC	1440
Ile	Ile	Pro	Ser	Ser	Gln	Ile	Thr	Gln	Ile	Pro	Leu	Thr	Lys	Ser	Thr	
			1675					1680					1685			
AAC	CTG	GGC	AGC	GGC	ACC	AGC	GTG	GTG	AAG	GGC	CCC	GGC	TTC	ACC	GGC	1488
Asn	Leu	Gly	Ser	Gly	Thr	Ser	Val	Val	Lys	Gly	Pro	Gly	Phe	Thr	Gly	
		1690					1695				1700					
GGC	GAC	ATC	CTG	CGC	CGC	ACC	AGC	CCC	GGC	CAG	ATC	AGC	ACC	CTG	CGC	1536
Gly	Asp	Ile	Leu	Arg	Arg	Thr	Ser	Pro	Gly	Gln	Ile	Ser	Thr	Leu	Arg	
		1705				1710					1715					
GTG	AAC	ATC	ACC	GCC	CCC	CTG	AGC	CAG	CGC	TAC	CGC	GTC	CGC	ATC	CGC	1584
Val	Asn	Ile	Thr	Ala	Pro	Leu	Ser	Gln	Arg	Tyr	Arg	Val	Arg	Ile	Arg	
		1720			1725					1730					1735	
TAC	GCC	AGC	ACC	ACC	AAC	CTG	CAG	TTC	CAC	ACC	AGC	ATC	GAC	GGC	CGC	1632
Tyr	Ala	Ser	Thr	Thr	Asn	Leu	Gln	Phe	His	Thr	Ser	Ile	Asp	Gly	Arg	
				1740					1745					1750		
CCC	ATC	AAC	CAG	GGC	AAC	TTC	AGC	GCC	ACC	ATG	AGC	AGC	GGC	AGC	AAC	1680
Pro	Ile	Asn	Gln	Gly	Asn	Phe	Ser	Ala	Thr	Met	Ser	Ser	Gly	Ser	Asn	
			1755					1760					1765			
CTG	CAG	AGC	GGC	AGC	TTC	CGC	ACC	GTG	GGC	TTC	ACC	ACC	CCC	TTC	AAC	1728

Leu	Gln	Ser	Gly	Ser	Phe	Arg	Thr	Val	Gly	Phe	Thr	Thr	Pro	Phe	Asn	
		1770						1775					1780			
TTC	AGC	AAC	GGC	AGC	AGC	GTG	TTC	ACC	CTG	AGC	GCC	CAC	GTG	TTC	AAC	1776
Phe	Ser	Asn	Gly	Ser	Ser	Val	Phe	Thr	Leu	Ser	Ala	His	Val	Phe	Asn	
	1785					1790				1795						
AGC	GGC	AAC	GAG	GTG	TAC	ATC	GAC	CGC	ATC	GAG	TTC	GTG	CCC	GCC	GAG	1824
Ser	Gly	Asn	Glu	Val	Tyr	Ile	Asp	Arg	Ile	Glu	Phe	Val	Pro	Ala	Glu	
1800					1805				1810						1815	
GTG	ACC	TTC	GAG	GCC	GAG	TAC	GAC	CTG	GAG	AGG	GCT	CAG	AAG	GCC	GTG	1872
Val	Thr	Phe	Glu	Ala	Glu	Tyr	Asp	Leu	Glu	Arg	Ala	Gln	Lys	Ala	Val	
				1820				1825						1830		
AAC	GAG	CTG	TTC	ACC	AGC	AGC	AAC	CAG	ATC	GGC	CTG	AAG	ACC	GAC	GTG	1920
Asn	Glu	Leu	Phe	Thr	Ser	Ser	Asn	Gln	Ile	Gly	Leu	Lys	Thr	Asp	Val	
			1835					1840					1845			
ACC	GAC	TAC	CAC	ATC	GAT	CAA	GTA	TCC	AAT	TTA	GTT	GAG	TGT	TTA	TCT	1968
Thr	Asp	Tyr	His	Ile	Asp	Gln	Val	Ser	Asn	Leu	Val	Glu	Cys	Leu	Ser	
		1850				1855						1860				
GAT	GAA	TTT	TGT	CTG	GAT	GAA	AAA	AAA	GAA	TTG	TCC	GAG	AAA	GTC	AAA	2016
Asp	Glu	Phe	Cys	Leu	Asp	Glu	Lys	Lys	Glu	Leu	Ser	Glu	Lys	Val	Lys	
	1865					1870					1875					
CAT	GCG	AAG	CGA	CTT	AGT	GAT	GAG	CGG	AAT	TTA	CTT	CAA	GAT	CCA	AAC	2064
His	Ala	Lys	Arg	Leu	Ser	Asp	Glu	Arg	Asn	Leu	Leu	Gln	Asp	Pro	Asn	
1880					1885				1890						1895	
TTT	AGA	GGG	ATC	AAT	AGA	CAA	CTA	GAC	CGT	GGC	TGG	AGA	GGA	AGT	ACG	2112
Phe	Arg	Gly	Ile	Asn	Arg	Gln	Leu	Asp	Arg	Gly	Trp	Arg	Gly	Ser	Thr	
				1900				1905						1910		
GAT	ATT	ACC	ATC	CAA	GGA	GGC	GAT	GAC	GTA	TTC	AAA	GAG	AAT	TAC	GTT	2160
Asp	Ile	Thr	Ile	Gln	Gly	Gly	Asp	Asp	Val	Phe	Lys	Glu	Asn	Tyr	Val	
			1915				1920					1925				
ACG	CTA	TTG	GGT	ACC	TTT	GAT	GAG	TGC	TAT	CCA	ACG	TAT	TTA	TAT	CAA	2208
Thr	Leu	Leu	Gly	Thr	Phe	Asp	Glu	Cys	Tyr	Pro	Thr	Tyr	Leu	Tyr	Gln	
		1930					1935					1940				
AAA	ATA	GAT	GAG	TCG	AAA	TTA	AAA	GCC	TAT	ACC	CGT	TAC	CAA	TTA	AGA	2256
Lys	Ile	Asp	Glu	Ser	Lys	Leu	Lys	Ala	Tyr	Thr	Arg	Tyr	Gln	Leu	Arg	
	1945					1950					1955					
GGG	TAT	ATC	GAA	GAT	AGT	CAA	GAC	TTA	GAA	ATC	TAT	TTA	ATT	CGC	TAC	2304
Gly	Tyr	Ile	Glu	Asp	Ser	Gln	Asp	Leu	Glu	Ile	Tyr	Leu	Ile	Arg	Tyr	
1960				1965					1970						1975	
AAT																

2010	2015	2020	
TTA GGT GTA TGG GTG ATA TTC AAG ATT AAG ACG CAA GAT GGC CAT GCA Leu Gly Val Trp Val Ile Phe Lys Ile Lys Thr Gln Asp Gly His Ala 2025 2030 2035			2496
AGA CTA GGA AAT CTA GAA TTT CTC GAA GAG AAA CCA TTA GTA GGA GAA Arg Leu Gly Asn Leu Glu Phe Leu Glu Glu Lys Pro Leu Val Gly Glu 2040 2045 2050 2055			2544
GCA CTA GCT CGT GTG AAA AGA GCG GAG AAA AAA TGG AGA GAC AAA CGT Ala Leu Ala Arg Val Lys Arg Ala Glu Lys Lys Trp Arg Asp Lys Arg 2060 2065 2070			2592
GAA AAA TTG GAA TGG GAA ACA AAT ATT GTT TAT AAA GAG GCA AAA GAA Glu Lys Leu Glu Trp Glu Thr Asn Ile Val Tyr Lys Glu Ala Lys Glu 2075 2080 2085			2640
TCT GTA GAT GCT TTA TTT GTA AAC TCT CAA TAT GAT AGA TTA CAA GCG Ser Val Asp Ala Leu Phe Val Asn Ser Gln Tyr Asp Arg Leu Gln Ala 2090 2095 2100			2688
GAT ACC AAC ATC GCG ATG ATT CAT GCG GCA GAT AAA CGC GTT CAT AGC Asp Thr Asn Ile Ala Met Ile His Ala Ala Asp Lys Arg Val His Ser 2105 2110 2115			2736
ATT CGA GAA GCT TAT CTG CCT GAG CTG TCT GTG ATT CCG GGT GTC AAT Ile Arg Glu Ala Tyr Leu Pro Glu Leu Ser Val Ile Pro Gly Val Asn 2120 2125 2130 2135			2784
GCG GCT ATT TTT GAA GAA TTA GAA GGG CGT ATT TTC ACT GCA TTC TCC Ala Ala Ile Phe Glu Glu Leu Glu Gly Arg Ile Phe Thr Ala Phe Ser 2140 2145 2150			2832
CTA TAT GAT GCG AGA AAT GTC ATT AAA AAT GGT GAT TTT AAT AAT GGC Leu Tyr Asp Ala Arg Asn Val Ile Lys Asn Gly Asp Phe Asn Asn Gly 2155 2160 2165			2880
TTA TCC TGC TGG AAC GTG AAA GGG CAT GTA GAT GTA GAA GAA CAA AAC Leu Ser Cys Trp Asn Val Lys Gly His Val Asp Val Glu Glu Gln Asn 2170 2175 2180			2928
AAC CAC CGT TCG GTC CTT GTT GTT CCG GAA TGG GAA GCA GAA GTG TCA Asn His Arg Ser Val Leu Val Val Pro Glu Trp Glu Ala Glu Val Ser 2185 2190 2195			2976
CAA GAA GTT CGT GTC TGT CCG GGT CGT GGC TAT ATC CTT CGT GTC ACA Gln Glu Val Arg Val Cys Pro Gly Arg Gly Tyr Ile Leu Arg Val Thr 2200 2205 2210 2215			3024
GCG TAC AAG GAG GGA TAT GGA GAA GGT TGC GTA ACC ATT CAT GAG ATC Ala Tyr Lys Glu Gly Tyr Gly Glu Gly Cys Val Thr Ile His Glu Ile 2220 2225 2230			3072
GAG AAC AAT ACA GAC GAA CTG AAG TTT AGC AAC TGT GTA GAA GAG GAA Glu Asn Asn Thr Asp Glu Leu Lys Phe Ser Asn Cys Val Glu Glu Glu 2235 2240 2245			3120
GTA TAT CCA AAC AAC ACG GTA ACG TGT AAT GAT TAT ACT GCG ACT CAA Val Tyr Pro Asn Asn Thr Val Thr Cys Asn Asp Tyr Thr Ala Thr Gln 2250 2255 2260			3168

GAA GAA TAT GAG GGT ACG TAC ACT TCT CGT AAT CGA GGA TAT GAC GGA Glu Glu Tyr Glu Gly Thr Tyr Thr Ser Arg Asn Arg Gly Tyr Asp Gly 2265 2270 2275	3216
GCC TAT GAA AGC AAT TCT TCT GTA CCA GCT GAT TAT GCA TCA GCC TAT Ala Tyr Glu Ser Asn Ser Ser Val Pro Ala Asp Tyr Ala Ser Ala Tyr 2280 2285 2290 2295	3264
GAA GAA AAA GCA TAT ACA GAT GGA CGA AGA GAC AAT CCT TGT GAA TCT Glu Glu Lys Ala Tyr Thr Asp Gly Arg Arg Asp Asn Pro Cys Glu Ser 2300 2305 2310	3312
AAC AGA GGA TAT GGG GAT TAC ACA CCA CTA CCA GCT GGC TAT GTG ACA Asn Arg Gly Tyr Gly Asp Tyr Thr Pro Leu Pro Ala Gly Tyr Val Thr 2315 2320 2325	3360
AAA GAA TTA GAG TAC TTC CCA GAA ACC GAT AAG GTA TGG ATT GAG ATC Lys Glu Leu Glu Tyr Phe Pro Glu Thr Asp Lys Val Trp Ile Glu Ile 2330 2335 2340	3408
GGA GAA ACG GAA GGA ACA TTC ATC GTG GAC AGC GTG GAA TTA CTT CTT Gly Glu Thr Glu Gly Thr Phe Ile Val Asp Ser Val Glu Leu Leu Leu 2345 2350 2355	3456
ATG GAG GAA TAA Met Glu Glu 2360	3468

(2) INFORMATION FOR SEQ ID NO:9:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1155 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

Met Asp Asn Asn Pro Asn Ile Asn Glu Cys Ile Pro Tyr Asn Cys Leu 1 5 10 15
Ser Asn Pro Glu Val Glu Val Leu Gly Gly Glu Arg Ile Glu Thr Gly 20 25 30
Tyr Thr Pro Ile Asp Ile Ser Leu Ser Leu Thr Gln Phe Leu Leu Ser 35 40 45
Glu Phe Val Pro Gly Ala Gly Phe Val Leu Gly Leu Val Asp Ile Ile 50 55 60
Trp Gly Ile Phe Gly Pro Ser Gln Trp Asp Ala Phe Leu Val Gln Ile 65 70 75 80
Glu Gln Leu Ile Asn Gln Arg Ile Glu Glu Phe Ala Arg Asn Gln Ala 85 90 95
Ile Ser Arg Leu Glu Gly Leu Ser Asn Leu Tyr Gln Ile Tyr Ala Glu 100 105 110

Val	Ser	Met	Phe	Arg	Ser	Gly	Phe	Ser	Asn	Ser	Ser	Val	Ser	Ile	Ile		
		435					440					445					
Arg	Ala	Pro	Met	Phe	Ser	Trp	Ile	His	Arg	Ser	Ala	Glu	Phe	Asn	Asn		
	450					455					460						
Ile	Ile	Pro	Ser	Ser	Gln	Ile	Thr	Gln	Ile	Pro	Leu	Thr	Lys	Ser	Thr		
465					470					475					480		
Asn	Leu	Gly	Ser	Gly	Thr	Ser	Val	Val	Lys	Gly	Pro	Gly	Phe	Thr	Gly		
				485					490					495			
Gly	Asp	Ile	Leu	Arg	Arg	Thr	Ser	Pro	Gly	Gln	Ile	Ser	Thr	Leu	Arg		
			500					505					510				
Val	Asn	Ile	Thr	Ala	Pro	Leu	Ser	Gln	Arg	Tyr	Arg	Val	Arg	Ile	Arg		
		515					520					525					
Tyr	Ala	Ser	Thr	Thr	Asn	Leu	Gln	Phe	His	Thr	Ser	Ile	Asp	Gly	Arg		
	530					535					540						
Pro	Ile	Asn	Gln	Gly	Asn	Phe	Ser	Ala	Thr	Met	Ser	Ser	Gly	Ser	Asn		
545					550					555					560		
Leu	Gln	Ser	Gly	Ser	Phe	Arg	Thr	Val	Gly	Phe	Thr	Thr	Pro	Phe	Asn		
				565					570					575			
Phe	Ser	Asn	Gly	Ser	Ser	Val	Phe	Thr	Leu	Ser	Ala	His	Val	Phe	Asn		
			580					585					590				
Ser	Gly	Asn	Glu	Val	Tyr	Ile	Asp	Arg	Ile	Glu	Phe	Val	Pro	Ala	Glu		
		595					600					605					
Val	Thr	Phe	Glu	Ala	Glu	Tyr	Asp	Leu	Glu	Arg	Ala	Gln	Lys	Ala	Val		
	610					615					620						
Asn	Glu	Leu	Phe	Thr	Ser	Ser	Asn	Gln	Ile	Gly	Leu	Lys	Thr	Asp	Val		
625					630					635					640		
Thr	Asp	Tyr	His	Ile	Asp	Gln	Val	Ser	Asn	Leu	Val	Glu	Cys	Leu	Ser		
				645				650						655			
Asp	Glu	Phe	Cys	Leu	Asp	Glu	Lys	Lys	Glu	Leu	Ser	Glu	Lys	Val	Lys		
			660					665					670				
His	Ala	Lys	Arg	Leu	Ser	Asp	Glu	Arg	Asn	Leu	Leu	Gln	Asp	Pro	Asn		
		675					680					685					
Phe	Arg	Gly	Ile	Asn	Arg	Gln	Leu	Asp	Arg	Gly	Trp	Arg	Gly	Ser	Thr		
	690					695					700						
Asp	Ile	Thr	Ile	Gln	Gly	Gly	Asp	Asp	Val	Phe	Lys	Glu	Asn	Tyr	Val		
705				710						715					720		
Thr	Leu	Leu	Gly	Thr	Phe	Asp	Glu	Cys	Tyr	Pro	Thr	Tyr	Leu	Tyr	Gln		
				725					730					735			
Lys	Ile	Asp	Glu	Ser	Lys	Leu	Lys	Ala	Tyr	Thr	Arg	Tyr	Gln	Leu	Arg		
		740						745					750				
Gly	Tyr	Ile	Glu	Asp	Ser	Gln	Asp	Leu	Glu	Ile	Tyr	Leu	Ile	Arg	Tyr		

755					760					765						
Asn	Ala	Lys	His	Glu	Thr	Val	Asn	Val	Pro	Gly	Thr	Gly	Ser	Leu	Trp	
770					775					780						
Pro	Leu	Ser	Ala	Pro	Ser	Pro	Ile	Gly	Lys	Cys	Ala	His	His	Ser	His	
785					790					795					800	
His	Phe	Ser	Leu	Asp	Ile	Asp	Val	Gly	Cys	Thr	Asp	Leu	Asn	Glu	Asp	
805					810					815						
Leu	Gly	Val	Trp	Val	Ile	Phe	Lys	Ile	Lys	Thr	Gln	Asp	Gly	His	Ala	
820					825					830						
Arg	Leu	Gly	Asn	Leu	Glu	Phe	Leu	Glu	Glu	Lys	Pro	Leu	Val	Gly	Glu	
835					840					845						
Ala	Leu	Ala	Arg	Val	Lys	Arg	Ala	Glu	Lys	Lys	Trp	Arg	Asp	Lys	Arg	
850					855					860						
Glu	Lys	Leu	Glu	Trp	Glu	Thr	Asn	Ile	Val	Tyr	Lys	Glu	Ala	Lys	Glu	
865					870					875					880	
Ser	Val	Asp	Ala	Leu	Phe	Val	Asn	Ser	Gln	Tyr	Asp	Arg	Leu	Gln	Ala	
885					890					895						
Asp	Thr	Asn	Ile	Ala	Met	Ile	His	Ala	Ala	Asp	Lys	Arg	Val	His	Ser	
900					905					910						
Ile	Arg	Glu	Ala	Tyr	Leu	Pro	Glu	Leu	Ser	Val	Ile	Pro	Gly	Val	Asn	
915					920					925						
Ala	Ala	Ile	Phe	Glu	Glu	Leu	Glu	Gly	Arg	Ile	Phe	Thr	Ala	Phe	Ser	
930					935					940						
Leu	Tyr	Asp	Ala	Arg	Asn	Val	Ile	Lys	Asn	Gly	Asp	Phe	Asn	Asn	Gly	
945					950					955					960	
Leu	Ser	Cys	Trp	Asn	Val	Lys	Gly	His	Val	Asp	Val	Glu	Glu	Gln	Asn	
965					970					975						
Asn	His	Arg	Ser	Val	Leu	Val	Val	Pro	Glu	Trp	Glu	Ala	Glu	Val	Ser	
980					985					990						
Gln	Glu	Val	Arg	Val	Cys	Pro	Gly	Arg	Gly	Tyr	Ile	Leu	Arg	Val	Thr	
995					1000					1005						
Ala	Tyr	Lys	Glu	Gly	Tyr	Gly	Glu	Gly	Cys	Val	Thr	Ile	His	Glu	Ile	
1010					1015					1020						
Glu	Asn	Asn	Thr	Asp	Glu	Leu	Lys	Phe	Ser	Asn	Cys	Val	Glu	Glu	Glu	
1025					1030					1035					1040	
Val	Tyr	Pro	Asn	Asn	Thr	Val	Thr	Cys	Asn	Asp	Tyr	Thr	Ala	Thr	Gln	
1045					1050					1055						
Glu	Glu	Tyr	Glu	Gly	Thr	Tyr	Thr	Ser	Arg	Asn	Arg	Gly	Tyr	Asp	Gly	
1060					1065					1070						
Ala	Tyr	Glu	Ser	Asn	Ser	Ser	Val	Pro	Ala	Asp	Tyr	Ala	Ser	Ala	Tyr	
1075					1080					1085						

Glu Glu Lys Ala Tyr Thr Asp Gly Arg Arg Asp Asn Pro Cys Glu Ser
 1090 1095 1100

Asn Arg Gly Tyr Gly Asp Tyr Thr Pro Leu Pro Ala Gly Tyr Val Thr
 1105 1110 1115 1120

Lys Glu Leu Glu Tyr Phe Pro Glu Thr Asp Lys Val Trp Ile Glu Ile
 1125 1130 1135

Gly Glu Thr Glu Gly Thr Phe Ile Val Asp Ser Val Glu Leu Leu Leu
 1140 1145 1150

Met Glu Glu
 1155

(2) INFORMATION FOR SEQ ID NO:10:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 3546 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

- (A) DESCRIPTION: /desc = "Synthetic DNA"

(iii) HYPOTHETICAL: NO

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1..3543
- (D) OTHER INFORMATION: /product= "Full-length, hybrid, maize optimized heat stable cryIA(b)"
- /note= "Disclosed in Figure 9 as contained in pCIB5511."

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

ATG GAC AAC AAC CCC AAC ATC AAC GAG TGC ATC CCC TAC AAC TGC CTG	48
Met Asp Asn Asn Pro Asn Ile Asn Glu Cys Ile Pro Tyr Asn Cys Leu	
1160 1165 1170	
AGC AAC CCC GAG GTG GAG GTG CTG GGC GGC GAG CGC ATC GAG ACC GGC	96
Ser Asn Pro Glu Val Glu Val Leu Gly Gly Glu Arg Ile Glu Thr Gly	
1175 1180 1185	
TAC ACC CCC ATC GAC ATC AGC CTG AGC CTG ACC CAG TTC CTG CTG AGC	144
Tyr Thr Pro Ile Asp Ile Ser Leu Ser Leu Thr Gln Phe Leu Leu Ser	
1190 1195 1200	
GAG TTC GTG CCC GGC GCC GGC TTC GTG CTG GGC CTG GTG GAC ATC ATC	192
Glu Phe Val Pro Gly Ala Gly Phe Val Leu Gly Leu Val Asp Ile Ile	
1205 1210 1215	
TGG GGC ATC TTC GGC CCC AGC CAG TGG GAC GCC TTC CTG GTG CAG ATC	240
Trp Gly Ile Phe Gly Pro Ser Gln Trp Asp Ala Phe Leu Val Gln Ile	
1220 1225 1230 1235	
GAG CAG CTG ATC AAC CAG CGC ATC GAG GAG TTC GCC CGC AAC CAG GCC	288

Glu Gln Leu Ile Asn Gln Arg Ile Glu Glu Phe Ala Arg Asn Gln Ala	1240	1245	1250	
ATC AGC CGC CTG GAG GGC CTG AGC AAC CTG TAC CAA ATC TAC GCC GAG	1255	1260	1265	336
Ile Ser Arg Leu Glu Gly Leu Ser Asn Leu Tyr Gln Ile Tyr Ala Glu				
AGC TTC CGC GAG TGG GAG GCC GAC CCC ACC AAC CCC GCC CTG CGC GAG	1270	1275	1280	384
Ser Phe Arg Glu Trp Glu Ala Asp Pro Thr Asn Pro Ala Leu Arg Glu				
GAG ATG CGC ATC CAG TTC AAC GAC ATG AAC AGC GCC CTG ACC ACC GCC	1285	1290	1295	432
Glu Met Arg Ile Gln Phe Asn Asp Met Asn Ser Ala Leu Thr Thr Ala				
ATC CCC CTG TTC GCC GTG CAG AAC TAC CAG GTG CCC CTG CTG AGC GTG	1300	1305	1310	480
Ile Pro Leu Phe Ala Val Gln Asn Tyr Gln Val Pro Leu Leu Ser Val				
TAC GTG CAG GCC GCC AAC CTG CAC CTG AGC GTG CTG CGC GAC GTC AGC	1320	1325	1330	528
Tyr Val Gln Ala Ala Asn Leu His Leu Ser Val Leu Arg Asp Val Ser				
GTG TTC GGC CAG CGC TGG GGC TTC GAC GCC GCC ACC ATC AAC AGC CGC	1335	1340	1345	576
Val Phe Gly Gln Arg Trp Gly Phe Asp Ala Ala Thr Ile Asn Ser Arg				
TAC AAC GAC CTG ACC CGC CTG ATC GGC AAC TAC ACC GAC CAC GCC GTG	1350	1355	1360	624
Tyr Asn Asp Leu Thr Arg Leu Ile Gly Asn Tyr Thr Asp His Ala Val				
CGC TGG TAC AAC ACC GGC CTG GAG CGC GTG TGG GGT CCC GAC AGC CGC	1365	1370	1375	672
Arg Trp Tyr Asn Thr Gly Leu Glu Arg Val Trp Gly Pro Asp Ser Arg				
GAC TGG ATC AGG TAC AAC CAG TTC CGC CGC GAG CTG ACC CTG ACC GTG	1380	1385	1390	720
Asp Trp Ile Arg Tyr Asn Gln Phe Arg Arg Glu Leu Thr Leu Thr Val				
CTG GAC ATC GTG AGC CTG TTC CCC AAC TAC GAC AGC CGC ACC TAC CCC	1400	1405	1410	768
Leu Asp Ile Val Ser Leu Phe Pro Asn Tyr Asp Ser Arg Thr Tyr Pro				
ATC CGC ACC GTG AGC CAG CTG ACC CGC GAG ATT TAC ACC AAC CCC GTG	1415	1420	1425	816
Ile Arg Thr Val Ser Gln Leu Thr Arg Glu Ile Tyr Thr Asn Pro Val				
CTG GAG AAC TTC GAC GGC AGC TTC CGC GGC AGC GCC CAG GGC ATC GAG	1430	1435	1440	864
Leu Glu Asn Phe Asp Gly Ser Phe Arg Gly Ser Ala Gln Gly Ile Glu				
GGC AGC ATC CGC AGC CCC CAC CTG ATG GAC ATC CTG AAC AGC ATC ACC	1445	1450	1455	912
Gly Ser Ile Arg Ser Pro His Leu Met Asp Ile Leu Asn Ser Ile Thr				
ATC TAC ACC GAC GCC CAC CGC GGC GAG TAC TAC TGG AGC GGC CAC CAG	1460	1465	1470	960
Ile Tyr Thr Asp Ala His Arg Gly Glu Tyr Tyr Trp Ser Gly His Gln				
ATC ATG GCC AGC CCC GTC GGC TTC AGC GGC CCC GAG TTC ACC TTC CCC				1008
Ile Met Ala Ser Pro Val Gly Phe Ser Gly Pro Glu Phe Thr Phe Pro				

1480	1485	1490	
CTG TAC GGC ACC ATG GGC AAC GCT GCA CCT CAG CAG CGC ATC GTG GCA Leu Tyr Gly Thr Met Gly Asn Ala Ala Pro Gln Gln Arg Ile Val Ala 1495 1500 1505			1056
CAG CTG GGC CAG GGA GTG TAC CGC ACC CTG AGC AGC ACC CTG TAC CGT Gln Leu Gly Gln Gly Val Tyr Arg Thr Leu Ser Ser Thr Leu Tyr Arg 1510 1515 1520			1104
CGA CCT TTC AAC ATC GGC ATC AAC AAC CAG CAG CTG AGC GTG CTG GAC Arg Pro Phe Asn Ile Gly Ile Asn Asn Gln Gln Leu Ser Val Leu Asp 1525 1530 1535			1152
GGC ACC GAG TTC GCC TAC GGC ACC AGC AGC AAC CTG CCC AGC GCC GTG Gly Thr Glu Phe Ala Tyr Gly Thr Ser Ser Asn Leu Pro Ser Ala Val 1540 1545 1550 1555			1200
TAC CGC AAG AGC GGC ACC GTG GAC AGC CTG GAC GAG ATC CCC CCT CAG Tyr Arg Lys Ser Gly Thr Val Asp Ser Leu Asp Glu Ile Pro Pro Gln 1560 1565 1570			1248
AAC AAC AAC GTG CCA CCT CGA CAG GGC TTC AGC CAC CGT CTG AGC CAC Asn Asn Asn Val Pro Pro Arg Gln Gly Phe Ser His Arg Leu Ser His 1575 1580 1585			1296
GTG AGC ATG TTC CGC AGT GGC TTC AGC AAC AGC AGC GTG AGC ATC ATC Val Ser Met Phe Arg Ser Gly Phe Ser Asn Ser Ser Val Ser Ile Ile 1590 1595 1600			1344
CGT GCA CCT ATG TTC AGC TGG ATT CAC CGC AGT GCC GAG TTC AAC AAC Arg Ala Pro Met Phe Ser Trp Ile His Arg Ser Ala Glu Phe Asn Asn 1605 1610 1615			1392
ATC ATC CCC AGC AGC CAG ATC ACC CAG ATC CCC CTG ACC AAG AGC ACC Ile Ile Pro Ser Ser Gln Ile Thr Gln Ile Pro Leu Thr Lys Ser Thr 1620 1625 1630 1635			1440
AAC CTG GGC AGC GGC ACC AGC GTG GTG AAG GGC CCC GGC TTC ACC GGC Asn Leu Gly Ser Gly Thr Ser Val Val Lys Gly Pro Gly Phe Thr Gly 1640 1645 1650			1488
GGC GAC ATC CTG CGC CGC ACC AGC CCC GGC CAG ATC AGC ACC CTG CGC Gly Asp Ile Leu Arg Arg Thr Ser Pro Gly Gln Ile Ser Thr Leu Arg 1655 1660 1665			1536
GTG AAC ATC ACC GCC CCC CTG AGC CAG CGC TAC CGC GTC CGC ATC CGC Val Asn Ile Thr Ala Pro Leu Ser Gln Arg Tyr Arg Val Arg Ile Arg 1670 1675 1680			1584
TAC GCC AGC ACC ACC AAC CTG CAG TTC CAC ACC AGC ATC GAC GGC CGC Tyr Ala Ser Thr Thr Asn Leu Gln Phe His Thr Ser Ile Asp Gly Arg 1685 1690 1695			1632
CCC ATC AAC CAG GGC AAC TTC AGC GCC ACC ATG AGC AGC GGC AGC AAC Pro Ile Asn Gln Gly Asn Phe Ser Ala Thr Met Ser Ser Gly Ser Asn 1700 1705 1710 1715			1680
CTG CAG AGC GGC AGC TTC CGC ACC GTG GGC TTC ACC ACC CCC TTC AAC Leu Gln Ser Gly Ser Phe Arg Thr Val Gly Phe Thr Thr Pro Phe Asn 1720 1725 1730			1728

TTC	AGC	AAC	GGC	AGC	AGC	GTG	TTC	ACC	CTG	AGC	GCC	CAC	GTG	TTC	AAC	1776
Phe	Ser	Asn	Gly	Ser	Ser	Val	Phe	Thr	Leu	Ser	Ala	His	Val	Phe	Asn	
			1735						1740						1745	
AGC	GGC	AAC	GAG	GTG	TAC	ATC	GAC	CGC	ATC	GAG	TTC	GTG	CCC	GCC	GAG	1824
Ser	Gly	Asn	Glu	Val	Tyr	Ile	Asp	Arg	Ile	Glu	Phe	Val	Pro	Ala	Glu	
			1750						1755					1760		
GTG	ACC	TTC	GAG	GCC	GAG	TAC	GAC	CTG	GAG	AGG	GCT	CAG	AAG	GCC	GTG	1872
Val	Thr	Phe	Glu	Ala	Glu	Tyr	Asp	Leu	Glu	Arg	Ala	Gln	Lys	Ala	Val	
			1765						1770						1775	
AAC	GAG	CTG	TTC	ACC	AGC	AGC	AAC	CAG	ATC	GGC	CTG	AAG	ACC	GAC	GTG	1920
Asn	Glu	Leu	Phe	Thr	Ser	Ser	Asn	Gln	Ile	Gly	Leu	Lys	Thr	Asp	Val	
						1785					1790				1795	
ACC	GAC	TAC	CAC	ATC	GAT	CAA	GTA	TCC	AAT	TTA	GTT	GAG	TGT	TTA	TCT	1968
Thr	Asp	Tyr	His	Ile	Asp	Gln	Val	Ser	Asn	Leu	Val	Glu	Cys	Leu	Ser	
						1800									1810	
GAT	GAA	TTT	TGT	CTG	GAT	GAA	AAA	AAA	GAA	TTG	TCC	GAG	AAA	GTC	AAA	2016
Asp	Glu	Phe	Cys	Leu	Asp	Glu	Lys	Lys	Glu	Leu	Ser	Glu	Lys	Val	Lys	
															1825	
CAT	GCG	AAG	CGA	CTT	AGT	GAT	GAG	CGG	AAT	TTA	CTT	CAA	GAT	CCA	AAC	2064
His	Ala	Lys	Arg	Leu	Ser	Asp	Glu	Arg	Asn	Leu	Leu	Gln	Asp	Pro	Asn	
															1840	
TTT	AGA	GGG	ATC	AAT	AGA	CAA	CTA	GAC	CGT	GGC	TGG	AGA	GGA	AGT	ACG	2112
Phe	Arg	Gly	Ile	Asn	Arg	Gln	Leu	Asp	Arg	Gly	Trp	Arg	Gly	Ser	Thr	
															1855	
GAT	ATT	ACC	ATC	CAA	GGA	GGC	GAT	GAC	GTA	TTC	AAA	GAG	AAT	TAC	GTT	2160
Asp	Ile	Thr	Ile	Gln	Gly	Gly	Asp	Asp	Val	Phe	Lys	Glu	Asn	Tyr	Val	
															1875	
ACG	CTA	TTG	GGT	ACC	TTC	GAC	GAG	TGC	TAC	CCC	ACC	TAC	CTG	TAC	CAG	2208
Thr	Leu	Leu	Gly	Thr	Phe	Asp	Glu	Cys	Tyr	Pro	Thr	Tyr	Leu	Tyr	Gln	
															1890	
AAG	ATC	GAC	GAG	AGC	AAG	CTG	AAG	GCC	TAC	ACC	CGC	TAC	CAG	CTG	CGC	2256
Lys	Ile	Asp	Glu	Ser	Lys	Leu	Lys	Ala	Tyr	Thr	Arg	Tyr	Gln	Leu	Arg	
															1905	
GGC	TAC	ATC	GAG	GAC	AGC	CAG	GAC	CTG	GAA	ATC	TAC	CTG	ATC	CGC	TAC	2304
Gly	Tyr	Ile	Glu	Asp	Ser	Gln	Asp	Leu	Glu	Ile	Tyr	Leu	Ile	Arg	Tyr	
															1920	
AAC	GCC	AAG	CAC	GAG	ACC	GTG	AAC	GTG	CCC	GGC	ACC	GGC	AGC	CTG	TGG	2352
Asn	Ala	Lys	His	Glu	Thr	Val	Asn	Val	Pro	Gly	Thr	Gly	Ser	Leu	Trp	
															1935	
CCC	CTG	AGC	GCC	CCC	AGC	CCC	ATC	GGC	AAG	TGC	GGG	GAG	CCG	AAT	CGA	2400
Pro	Leu	Ser	Ala	Pro	Ser	Pro	Ile	Gly	Lys	Cys	Gly	Glu	Pro	Asn	Arg	
															1955	
TGC	GCT	CCG	CAC	CTG	GAG	TGG	AAC	CCG	GAC	CTA	GAC	TGC	AGC	TGC	AGG	2448
Cys	Ala	Pro	His	Leu	Glu	Trp	Asn	Pro	Asp	Leu	Asp	Cys	Ser	Cys	Arg	
															1970	

GAC GGG GAG AAG TGC GCC CAC CAC AGC CAC CAC TTC AGC CTG GAC ATC Asp Gly Glu Lys Cys Ala His His Ser His His Phe Ser Leu Asp Ile 1975 1980 1985	2496
GAC GTG GGC TGC ACC GAC CTG AAC GAG GAC CTG GGC GTG TGG GTG ATC Asp Val Gly Cys Thr Asp Leu Asn Glu Asp Leu Gly Val Trp Val Ile 1990 1995 2000	2544
TTC AAG ATC AAG ACC CAG GAC GGC CAC GCC CGC CTG GGC AAT CTA GAA Phe Lys Ile Lys Thr Gln Asp Gly His Ala Arg Leu Gly Asn Leu Glu 2005 2010 2015	2592
TTT CTC GAA GAG AAA CCA TTA GTA GGA GAA GCA CTA GCT CGT GTG AAA Phe Leu Glu Glu Lys Pro Leu Val Gly Glu Ala Leu Ala Arg Val Lys 2020 2025 2030 2035	2640
AGA GCG GAG AAA AAA TGG AGA GAC AAA CGT GAA AAA TTG GAA TGG GAA Arg Ala Glu Lys Lys Trp Arg Asp Lys Arg Glu Lys Leu Glu Trp Glu 2040 2045 2050	2688
ACA AAT ATT GTT TAT AAA GAG GCA AAA GAA TCT GTA GAT GCT TTA TTT Thr Asn Ile Val Tyr Lys Glu Ala Lys Glu Ser Val Asp Ala Leu Phe 2055 2060 2065	2736
GTA AAC TCT CAA TAT GAT AGA TTA CAA GCG GAT ACC AAC ATC GCG ATG Val Asn Ser Gln Tyr Asp Arg Leu Gln Ala Asp Thr Asn Ile Ala Met 2070 2075 2080	2784
ATT CAT GCG GCA GAT AAA CGC GTT CAT AGC ATT CGA GAA GCT TAT CTG Ile His Ala Ala Asp Lys Arg Val His Ser Ile Arg Glu Ala Tyr Leu 2085 2090 2095	2832
CCT GAG CTG TCT GTG ATT CCG GGT GTC AAT GCG GCT ATT TTT GAA GAA Pro Glu Leu Ser Val Ile Pro Gly Val Asn Ala Ala Ile Phe Glu Glu 2100 2105 2110 2115	2880
TTA GAA GGG CGT ATT TTC ACT GCA TTC TCC CTA TAT GAT GCG AGA AAT Leu Glu Gly Arg Ile Phe Thr Ala Phe Ser Leu Tyr Asp Ala Arg Asn 2120 2125 2130	2928
GTC ATT AAA AAT GGT GAT TTT AAT AAT GGC TTA TCC TGC TGG AAC GTG Val Ile Lys Asn Gly Asp Phe Asn Asn Gly Leu Ser Cys Trp Asn Val 2135 2140 2145	2976
AAA GGG CAT GTA GAT GTA GAA GAA CAA AAC AAC CAC CGT TCG GTC CTT Lys Gly His Val Asp Val Glu Glu Gln Asn Asn His Arg Ser Val Leu 2150 2155 2160	3024
GTT GTT CCG GAA TGG GAA GCA GAA GTG TCA CAA GAA GTT CGT GTC TGT Val Val Pro Glu Trp Glu Ala Glu Val Ser Gln Glu Val Arg Val Cys 2165 2170 2175	3072
CCG GGT CGT GGC TAT ATC CTT CGT GTC ACA GCG TAC AAG GAG GGA TAT Pro Gly Arg Gly Tyr Ile Leu Arg Val Thr Ala Tyr Lys Glu Gly Tyr 2180 2185 2190 2195	3120
GGA GAA GGT TGC GTA ACC ATT CAT GAG ATC GAG AAC AAT ACA GAC GAA Gly Glu Gly Cys Val Thr Ile His Glu Ile Glu Asn Asn Thr Asp Glu 2200 2205 2210	3168
CTG AAG TTT AGC AAC TGT GTA GAA GAG GAA GTA TAT CCA AAC AAC ACG	3216

Leu Lys Phe Ser Asn Cys Val Glu Glu Glu Val Tyr Pro Asn Asn Thr
 2215 2220 2225

GTA ACG TGT AAT GAT TAT ACT GCG ACT CAA GAA GAA TAT GAG GGT ACG 3264
 Val Thr Cys Asn Asp Tyr Thr Ala Thr Gln Glu Glu Tyr Glu Gly Thr
 2230 2235 2240

TAC ACT TCT CGT AAT CGA GGA TAT GAC GGA GCC TAT GAA AGC AAT TCT 3312
 Tyr Thr Ser Arg Asn Arg Gly Tyr Asp Gly Ala Tyr Glu Ser Asn Ser
 2245 2250 2255

TCT GTA CCA GCT GAT TAT GCA TCA GCC TAT GAA GAA AAA GCA TAT ACA 3360
 Ser Val Pro Ala Asp Tyr Ala Ser Ala Tyr Glu Glu Lys Ala Tyr Thr
 2260 2265 2270 2275

GAT GGA CGA AGA GAC AAT CCT TGT GAA TCT AAC AGA GGA TAT GGG GAT 3408
 Asp Gly Arg Arg Asp Asn Pro Cys Glu Ser Asn Arg Gly Tyr Gly Asp
 2280 2285 2290

TAC ACA CCA CTA CCA GCT GGC TAT GTG ACA AAA GAA TTA GAG TAC TTC 3456
 Tyr Thr Pro Leu Pro Ala Gly Tyr Val Thr Lys Glu Leu Glu Tyr Phe
 2295 2300 2305

CCA GAA ACC GAT AAG GTA TGG ATT GAG ATC GGA GAA ACG GAA GGA ACA 3504
 Pro Glu Thr Asp Lys Val Trp Ile Glu Ile Gly Glu Thr Glu Gly Thr
 2310 2315 2320

TTC ATC GTG GAC AGC GTG GAA TTA CTT CTT ATG GAG GAA TAA 3546
 Phe Ile Val Asp Ser Val Glu Leu Leu Leu Met Glu Glu
 2325 2330 2335

(2) INFORMATION FOR SEQ ID NO:11:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1181 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

Met Asp Asn Asn Pro Asn Ile Asn Glu Cys Ile Pro Tyr Asn Cys Leu
 1 5 10 15

Ser Asn Pro Glu Val Glu Val Leu Gly Gly Glu Arg Ile Glu Thr Gly
 20 25 30

Tyr Thr Pro Ile Asp Ile Ser Leu Ser Leu Thr Gln Phe Leu Leu Ser
 35 40 45

Glu Phe Val Pro Gly Ala Gly Phe Val Leu Gly Leu Val Asp Ile Ile
 50 55 60

Trp Gly Ile Phe Gly Pro Ser Gln Trp Asp Ala Phe Leu Val Gln Ile
 65 70 75 80

Glu Gln Leu Ile Asn Gln Arg Ile Glu Glu Phe Ala Arg Asn Gln Ala
 85 90 95

Ile Ser Arg Leu Glu Gly Leu Ser Asn Leu Tyr Gln Ile Tyr Ala Glu
100 105 110

Ser Phe Arg Glu Trp Glu Ala Asp Pro Thr Asn Pro Ala Leu Arg Glu
115 120 125

Glu Met Arg Ile Gln Phe Asn Asp Met Asn Ser Ala Leu Thr Thr Ala
130 135 140

Ile Pro Leu Phe Ala Val Gln Asn Tyr Gln Val Pro Leu Leu Ser Val
145 150 155 160

Tyr Val Gln Ala Ala Asn Leu His Leu Ser Val Leu Arg Asp Val Ser
165 170 175

Val Phe Gly Gln Arg Trp Gly Phe Asp Ala Ala Thr Ile Asn Ser Arg
180 185 190

Tyr Asn Asp Leu Thr Arg Leu Ile Gly Asn Tyr Thr Asp His Ala Val
195 200 205

Arg Trp Tyr Asn Thr Gly Leu Glu Arg Val Trp Gly Pro Asp Ser Arg
210 215 220

Asp Trp Ile Arg Tyr Asn Gln Phe Arg Arg Glu Leu Thr Leu Thr Val
225 230 235 240

Leu Asp Ile Val Ser Leu Phe Pro Asn Tyr Asp Ser Arg Thr Tyr Pro
245 250 255

Ile Arg Thr Val Ser Gln Leu Thr Arg Glu Ile Tyr Thr Asn Pro Val
260 265 270

Leu Glu Asn Phe Asp Gly Ser Phe Arg Gly Ser Ala Gln Gly Ile Glu
275 280 285

Gly Ser Ile Arg Ser Pro His Leu Met Asp Ile Leu Asn Ser Ile Thr
290 295 300

Ile Tyr Thr Asp Ala His Arg Gly Glu Tyr Tyr Trp Ser Gly His Gln
305 310 315 320

Ile Met Ala Ser Pro Val Gly Phe Ser Gly Pro Glu Phe Thr Phe Pro
325 330 335

Leu Tyr Gly Thr Met Gly Asn Ala Ala Pro Gln Gln Arg Ile Val Ala
340 345 350

Gln Leu Gly Gln Gly Val Tyr Arg Thr Leu Ser Ser Thr Leu Tyr Arg
355 360 365

Arg Pro Phe Asn Ile Gly Ile Asn Asn Gln Gln Leu Ser Val Leu Asp
370 375 380

Gly Thr Glu Phe Ala Tyr Gly Thr Ser Ser Asn Leu Pro Ser Ala Val
385 390 395 400

Tyr Arg Lys Ser Gly Thr Val Asp Ser Leu Asp Glu Ile Pro Pro Gln
405 410 415

Asn Asn Asn Val Pro Pro Arg Gln Gly Phe Ser His Arg Leu Ser His

420					425					430					
Val	Ser	Met	Phe	Arg	Ser	Gly	Phe	Ser	Asn	Ser	Ser	Val	Ser	Ile	Ile
		435					440					445			
Arg	Ala	Pro	Met	Phe	Ser	Trp	Ile	His	Arg	Ser	Ala	Glu	Phe	Asn	Asn
	450					455					460				
Ile	Ile	Pro	Ser	Ser	Gln	Ile	Thr	Gln	Ile	Pro	Leu	Thr	Lys	Ser	Thr
465					470					475					480
Asn	Leu	Gly	Ser	Gly	Thr	Ser	Val	Val	Lys	Gly	Pro	Gly	Phe	Thr	Gly
				485					490					495	
Gly	Asp	Ile	Leu	Arg	Arg	Thr	Ser	Pro	Gly	Gln	Ile	Ser	Thr	Leu	Arg
			500					505					510		
Val	Asn	Ile	Thr	Ala	Pro	Leu	Ser	Gln	Arg	Tyr	Arg	Val	Arg	Ile	Arg
		515					520					525			
Tyr	Ala	Ser	Thr	Thr	Asn	Leu	Gln	Phe	His	Thr	Ser	Ile	Asp	Gly	Arg
	530					535					540				
Pro	Ile	Asn	Gln	Gly	Asn	Phe	Ser	Ala	Thr	Met	Ser	Ser	Gly	Ser	Asn
545					550					555					560
Leu	Gln	Ser	Gly	Ser	Phe	Arg	Thr	Val	Gly	Phe	Thr	Thr	Pro	Phe	Asn
				565					570					575	
Phe	Ser	Asn	Gly	Ser	Ser	Val	Phe	Thr	Leu	Ser	Ala	His	Val	Phe	Asn
			580				585					590			
Ser	Gly	Asn	Glu	Val	Tyr	Ile	Asp	Arg	Ile	Glu	Phe	Val	Pro	Ala	Glu
		595					600					605			
Val	Thr	Phe	Glu	Ala	Glu	Tyr	Asp	Leu	Glu	Arg	Ala	Gln	Lys	Ala	Val
	610					615					620				
Asn	Glu	Leu	Phe	Thr	Ser	Ser	Asn	Gln	Ile	Gly	Leu	Lys	Thr	Asp	Val
625					630					635					640
Thr	Asp	Tyr	His	Ile	Asp	Gln	Val	Ser	Asn	Leu	Val	Glu	Cys	Leu	Ser
				645					650					655	
Asp	Glu	Phe	Cys	Leu	Asp	Glu	Lys	Lys	Glu	Leu	Ser	Glu	Lys	Val	Lys
			660					665					670		
His	Ala	Lys	Arg	Leu	Ser	Asp	Glu	Arg	Asn	Leu	Leu	Gln	Asp	Pro	Asn
		675					680					685			
Phe	Arg	Gly	Ile	Asn	Arg	Gln	Leu	Asp	Arg	Gly	Trp	Arg	Gly	Ser	Thr
	690					695					700				
Asp	Ile	Thr	Ile	Gln	Gly	Gly	Asp	Asp	Val	Phe	Lys	Glu	Asn	Tyr	Val
705					710					715					720
Thr	Leu	Leu	Gly	Thr	Phe	Asp	Glu	Cys	Tyr	Pro	Thr	Tyr	Leu	Tyr	Gln
				725					730					735	
Lys	Ile	Asp	Glu	Ser	Lys	Leu	Lys	Ala	Tyr	Thr	Arg	Tyr	Gln	Leu	Arg
			740					745					750		

Gly	Tyr	Ile	Glu	Asp	Ser	Gln	Asp	Leu	Glu	Ile	Tyr	Leu	Ile	Arg	Tyr
		755					760					765			
Asn	Ala	Lys	His	Glu	Thr	Val	Asn	Val	Pro	Gly	Thr	Gly	Ser	Leu	Trp
		770					775					780			
Pro	Leu	Ser	Ala	Pro	Ser	Pro	Ile	Gly	Lys	Cys	Gly	Glu	Pro	Asn	Arg
		785					790				795				800
Cys	Ala	Pro	His	Leu	Glu	Trp	Asn	Pro	Asp	Leu	Asp	Cys	Ser	Cys	Arg
				805						810				815	
Asp	Gly	Glu	Lys	Cys	Ala	His	His	Ser	His	His	Phe	Ser	Leu	Asp	Ile
			820						825				830		
Asp	Val	Gly	Cys	Thr	Asp	Leu	Asn	Glu	Asp	Leu	Gly	Val	Trp	Val	Ile
			835					840					845		
Phe	Lys	Ile	Lys	Thr	Gln	Asp	Gly	His	Ala	Arg	Leu	Gly	Asn	Leu	Glu
			850				855					860			
Phe	Leu	Glu	Glu	Lys	Pro	Leu	Val	Gly	Glu	Ala	Leu	Ala	Arg	Val	Lys
			865				870				875				880
Arg	Ala	Glu	Lys	Lys	Trp	Arg	Asp	Lys	Arg	Glu	Lys	Leu	Glu	Trp	Glu
				885						890				895	
Thr	Asn	Ile	Val	Tyr	Lys	Glu	Ala	Lys	Glu	Ser	Val	Asp	Ala	Leu	Phe
			900						905					910	
Val	Asn	Ser	Gln	Tyr	Asp	Arg	Leu	Gln	Ala	Asp	Thr	Asn	Ile	Ala	Met
			915					920					925		
Ile	His	Ala	Ala	Asp	Lys	Arg	Val	His	Ser	Ile	Arg	Glu	Ala	Tyr	Leu
			930				935					940			
Pro	Glu	Leu	Ser	Val	Ile	Pro	Gly	Val	Asn	Ala	Ala	Ile	Phe	Glu	Glu
					950						955				960
Leu	Glu	Gly	Arg	Ile	Phe	Thr	Ala	Phe	Ser	Leu	Tyr	Asp	Ala	Arg	Asn
				965						970				975	
Val	Ile	Lys	Asn	Gly	Asp	Phe	Asn	Asn	Gly	Leu	Ser	Cys	Trp	Asn	Val
			980						985					990	
Lys	Gly	His	Val	Asp	Val	Glu	Glu	Gln	Asn	Asn	His	Arg	Ser	Val	Leu
			995					1000					1005		
Val	Val	Pro	Glu	Trp	Glu	Ala	Glu	Val	Ser	Gln	Glu	Val	Arg	Val	Cys
						1010						1020			
Pro	Gly	Arg	Gly	Tyr	Ile	Leu	Arg	Val	Thr	Ala	Tyr	Lys	Glu	Gly	Tyr
					1030						1035				1040
Gly	Glu	Gly	Cys	Val	Thr	Ile	His	Glu	Ile	Glu	Asn	Asn	Thr	Asp	Glu
				1045						1050				1055	
Leu	Lys	Phe	Ser	Asn	Cys	Val	Glu	Glu	Glu	Val	Tyr	Pro	Asn	Asn	Thr
				1060					1065					1070	

Val Thr Cys Asn Asp Tyr Thr Ala Thr Gln Glu Glu Tyr Glu Gly Thr
1075 1080 1085

Tyr Thr Ser Arg Asn Arg Gly Tyr Asp Gly Ala Tyr Glu Ser Asn Ser
1090 1095 1100

Ser Val Pro Ala Asp Tyr Ala Ser Ala Tyr Glu Glu Lys Ala Tyr Thr
1105 1110 1115 1120

Asp Gly Arg Arg Asp Asn Pro Cys Glu Ser Asn Arg Gly Tyr Gly Asp
1125 1130 1135

Tyr Thr Pro Leu Pro Ala Gly Tyr Val Thr Lys Glu Leu Glu Tyr Phe
1140 1145 1150

Pro Glu Thr Asp Lys Val Trp Ile Glu Ile Gly Glu Thr Glu Gly Thr
1155 1160 1165

Phe Ile Val Asp Ser Val Glu Leu Leu Leu Met Glu Glu
1170 1175 1180

(2) INFORMATION FOR SEQ ID NO:12:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 3546 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

- (A) DESCRIPTION: /desc = "Synthetic DNA"

(iii) HYPOTHETICAL: NO

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1..3543
- (D) OTHER INFORMATION: /product= "Full-length, hybrid, maize optimized heat stable cryIA(b)"
- /note= "Disclosed in Figure 11 as contained in pCIB5512"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

ATG GAC AAC AAC CCC AAC ATC AAC GAG TGC ATC CCC TAC AAC TGC CTG	48
Met Asp Asn Asn Pro Asn Ile Asn Glu Cys Ile Pro Tyr Asn Cys Leu	
1185 1190 1195	
AGC AAC CCC GAG GTG GAG GTG CTG GGC GGC GAG CGC ATC GAG ACC GGC	96
Ser Asn Pro Glu Val Glu Val Leu Gly Gly Glu Arg Ile Glu Thr Gly	
1200 1205 1210	
TAC ACC CCC ATC GAC ATC AGC CTG AGC CTG ACC CAG TTC CTG CTG AGC	144
Tyr Thr Pro Ile Asp Ile Ser Leu Ser Leu Thr Gln Phe Leu Leu Ser	
1215 1220 1225	
GAG TTC GTG CCC GGC GCC GGC TTC GTG CTG GGC CTG GTG GAC ATC ATC	192
Glu Phe Val Pro Gly Ala Gly Phe Val Leu Gly Leu Val Asp Ile Ile	
1230 1235 1240 1245	

TGG GGC ATC TTC GGC CCC AGC CAG TGG GAC GCC TTC CTG GTG CAG ATC Trp Gly Ile Phe Gly Pro Ser Gln Trp Asp Ala Phe Leu Val Gln Ile 1250 1255 1260	240
GAG CAG CTG ATC AAC CAG CGC ATC GAG GAG TTC GCC CGC AAC CAG GCC Glu Gln Leu Ile Asn Gln Arg Ile Glu Glu Phe Ala Arg Asn Gln Ala 1265 1270 1275	288
ATC AGC CGC CTG GAG GGC CTG AGC AAC CTG TAC CAA ATC TAC GCC GAG Ile Ser Arg Leu Glu Gly Leu Ser Asn Leu Tyr Gln Ile Tyr Ala Glu 1280 1285 1290	336
AGC TTC CGC GAG TGG GAG GCC GAC CCC ACC AAC CCC GCC CTG CGC GAG Ser Phe Arg Glu Trp Glu Ala Asp Pro Thr Asn Pro Ala Leu Arg Glu 1295 1300 1305	384
GAG ATG CGC ATC CAG TTC AAC GAC ATG AAC AGC GCC CTG ACC ACC GCC Glu Met Arg Ile Gln Phe Asn Asp Met Asn Ser Ala Leu Thr Thr Ala 1310 1315 1320 1325	432
ATC CCC CTG TTC GCC GTG CAG AAC TAC CAG GTG CCC CTG CTG AGC GTG Ile Pro Leu Phe Ala Val Gln Asn Tyr Gln Val Pro Leu Leu Ser Val 1330 1335 1340	480
TAC GTG CAG GCC GCC AAC CTG CAC CTG AGC GTG CTG CGC GAC GTC AGC Tyr Val Gln Ala Ala Asn Leu His Leu Ser Val Leu Arg Asp Val Ser 1345 1350 1355	528
GTG TTC GGC CAG CGC TGG GGC TTC GAC GCC GCC ACC ATC AAC AGC CGC Val Phe Gly Gln Arg Trp Gly Phe Asp Ala Ala Thr Ile Asn Ser Arg 1360 1365 1370	576
TAC AAC GAC CTG ACC CGC CTG ATC GGC AAC TAC ACC GAC CAC GCC GTG Tyr Asn Asp Leu Thr Arg Leu Ile Gly Asn Tyr Thr Asp His Ala Val 1375 1380 1385	624
CGC TGG TAC AAC ACC GGC CTG GAG CGC GTG TGG GGT CCC GAC AGC CGC Arg Trp Tyr Asn Thr Gly Leu Glu Arg Val Trp Gly Pro Asp Ser Arg 1390 1395 1400 1405	672
GAC TGG ATC AGG TAC AAC CAG TTC CGC CGC GAG CTG ACC CTG ACC GTG Asp Trp Ile Arg Tyr Asn Gln Phe Arg Arg Glu Leu Thr Leu Thr Val 1410 1415 1420	720
CTG GAC ATC GTG AGC CTG TTC CCC AAC TAC GAC AGC CGC ACC TAC CCC Leu Asp Ile Val Ser Leu Phe Pro Asn Tyr Asp Ser Arg Thr Tyr Pro 1425 1430 1435	768
ATC CGC ACC GTG AGC CAG CTG ACC CGC GAG ATT TAC ACC AAC CCC GTG Ile Arg Thr Val Ser Gln Leu Thr Arg Glu Ile Tyr Thr Asn Pro Val 1440 1445 1450	816
CTG GAG AAC TTC GAC GGC AGC TTC CGC GGC AGC GCC CAG GGC ATC GAG Leu Glu Asn Phe Asp Gly Ser Phe Arg Gly Ser Ala Gln Gly Ile Glu 1455 1460 1465	864
GGC AGC ATC CGC AGC CCC CAC CTG ATG GAC ATC CTG AAC AGC ATC ACC Gly Ser Ile Arg Ser Pro His Leu Met Asp Ile Leu Asn Ser Ile Thr 1470 1475 1480 1485	912
ATC TAC ACC GAC GCC CAC CGC GGC GAG TAC TAC TGG AGC GGC CAC CAG	960

Ile	Tyr	Thr	Asp	Ala	His	Arg	Gly	Glu	Tyr	Tyr	Trp	Ser	Gly	His	Gln	
				1490					1495					1500		
ATC	ATG	GCC	AGC	CCC	GTC	GGC	TTC	AGC	GGC	CCC	GAG	TTC	ACC	TTC	CCC	1008
Ile	Met	Ala	Ser	Pro	Val	Gly	Phe	Ser	Gly	Pro	Glu	Phe	Thr	Phe	Pro	
			1505					1510					1515			
CTG	TAC	GGC	ACC	ATG	GGC	AAC	GCT	GCA	CCT	CAG	CAG	CGC	ATC	GTG	GCA	1056
Leu	Tyr	Gly	Thr	Met	Gly	Asn	Ala	Ala	Pro	Gln	Gln	Arg	Ile	Val	Ala	
		1520					1525					1530				
CAG	CTG	GGC	CAG	GGA	GTG	TAC	CGC	ACC	CTG	AGC	AGC	ACC	CTG	TAC	CGT	1104
Gln	Leu	Gly	Gln	Gly	Val	Tyr	Arg	Thr	Leu	Ser	Ser	Thr	Leu	Tyr	Arg	
	1535					1540					1545					
CGA	CCT	TTC	AAC	ATC	GGC	ATC	AAC	AAC	CAG	CAG	CTG	AGC	GTG	CTG	GAC	1152
Arg	Pro	Phe	Asn	Ile	Gly	Ile	Asn	Asn	Gln	Gln	Leu	Ser	Val	Leu	Asp	
1550				1555					1560						1565	
GGC	ACC	GAG	TTC	GCC	TAC	GGC	ACC	AGC	AGC	AAC	CTG	CCC	AGC	GCC	GTG	1200
Gly	Thr	Glu	Phe	Ala	Tyr	Gly	Thr	Ser	Ser	Asn	Leu	Pro	Ser	Ala	Val	
				1570				1575						1580		
TAC	CGC	AAG	AGC	GGC	ACC	GTG	GAC	AGC	CTG	GAC	GAG	ATC	CCC	CCT	CAG	1248
Tyr	Arg	Lys	Ser	Gly	Thr	Val	Asp	Ser	Leu	Asp	Glu	Ile	Pro	Pro	Gln	
			1585					1590					1595			
AAC	AAC	AAC	GTG	CCA	CCT	CGA	CAG	GGC	TTC	AGC	CAC	CGT	CTG	AGC	CAC	1296
Asn	Asn	Asn	Val	Pro	Pro	Arg	Gln	Gly	Phe	Ser	His	Arg	Leu	Ser	His	
		1600					1605					1610				
GTG	AGC	ATG	TTC	CGC	AGT	GGC	TTC	AGC	AAC	AGC	AGC	GTG	AGC	ATC	ATC	1344
Val	Ser	Met	Phe	Arg	Ser	Gly	Phe	Ser	Asn	Ser	Ser	Val	Ser	Ile	Ile	
	1615					1620					1625					
CGT	GCA	CCT	ATG	TTC	AGC	TGG	ATT	CAC	CGC	AGT	GCC	GAG	TTC	AAC	AAC	1392
Arg	Ala	Pro	Met	Phe	Ser	Trp	Ile	His	Arg	Ser	Ala	Glu	Phe	Asn	Asn	
1630					1635				1640					1645		
ATC	ATC	CCC	AGC	AGC	CAG	ATC	ACC	CAG	ATC	CCC	CTG	ACC	AAG	AGC	ACC	1440
Ile	Ile	Pro	Ser	Ser	Gln	Ile	Thr	Gln	Ile	Pro	Leu	Thr	Lys	Ser	Thr	
				1650				1655						1660		
AAC	CTG	GGC	AGC	GGC	ACC	AGC	GTG	GTG	AAG	GGC	CCC	GGC	TTC	ACC	GGC	1488
Asn	Leu	Gly	Ser	Gly	Thr	Ser	Val	Val	Lys	Gly	Pro	Gly	Phe	Thr	Gly	
		1665					1670						1675			
GGC	GAC	ATC	CTG	CGC	CGC	ACC	AGC	CCC	GGC	CAG	ATC	AGC	ACC	CTG	CGC	1536
Gly	Asp	Ile	Leu	Arg	Arg	Thr	Ser	Pro	Gly	Gln	Ile	Ser	Thr	Leu	Arg	
		1680					1685					1690				
GTG	AAC	ATC	ACC	GCC	CCC	CTG	AGC	CAG	CGC	TAC	CGC	GTC	CGC	ATC	CGC	1584
Val	Asn	Ile	Thr	Ala	Pro	Leu	Ser	Gln	Arg	Tyr	Arg	Val	Arg	Ile	Arg	
	1695					1700					1705					
TAC	GCC	AGC	ACC	ACC	AAC	CTG	CAG	TTC	CAC	ACC	AGC	ATC	GAC	GGC	CGC	1632
Tyr	Ala	Ser	Thr	Thr	Asn	Leu	Gln	Phe	His	Thr	Ser	Ile	Asp	Gly	Arg	
1710					1715				1720					1725		
CCC	ATC	AAC	CAG	GGC	AAC	TTC	AGC	GCC	ACC	ATG	AGC	AGC	GGC	AGC	AAC	1680
Pro	Ile	Asn	Gln	Gly	Asn	Phe	Ser	Ala	Thr	Met	Ser	Ser	Gly	Ser	Asn	

1730										1735										1740										
CTG	CAG	AGC	GGC	AGC	TTC	CGC	ACC	GTG	GGC	TTC	ACC	ACC	CCC	TTC	AAC														1728	
Leu	Gln	Ser	Gly	Ser	Phe	Arg	Thr	Val	Gly	Phe	Thr	Thr	Pro	Phe	Asn															
			1745						1750					1755																
TTC	AGC	AAC	GGC	AGC	AGC	GTG	TTC	ACC	CTG	AGC	GCC	CAC	GTG	TTC	AAC														1776	
Phe	Ser	Asn	Gly	Ser	Ser	Val	Phe	Thr	Leu	Ser	Ala	His	Val	Phe	Asn															
			1760					1765					1770																	
AGC	GGC	AAC	GAG	GTG	TAC	ATC	GAC	CGC	ATC	GAG	TTC	GTG	CCC	GCC	GAG														1824	
Ser	Gly	Asn	Glu	Val	Tyr	Ile	Asp	Arg	Ile	Glu	Phe	Val	Pro	Ala	Glu															
			1775				1780						1785																	
GTG	ACC	TTC	GAG	GCC	GAG	TAC	GAC	CTG	GAG	AGG	GCT	CAG	AAG	GCC	GTG														1872	
Val	Thr	Phe	Glu	Ala	Glu	Tyr	Asp	Leu	Glu	Arg	Ala	Gln	Lys	Ala	Val															
						1795				1800					1805															
AAC	GAG	CTG	TTC	ACC	AGC	AGC	AAC	CAG	ATC	GGC	CTG	AAG	ACC	GAC	GTG														1920	
Asn	Glu	Leu	Phe	Thr	Ser	Ser	Asn	Gln	Ile	Gly	Leu	Lys	Thr	Asp	Val															
				1810					1815					1820																
ACC	GAC	TAC	CAC	ATC	GAT	CAG	GTG	AGC	AAC	CTG	GTG	GAG	TGC	TTA	AGC														1968	
Thr	Asp	Tyr	His	Ile	Asp	Gln	Val	Ser	Asn	Leu	Val	Glu	Cys	Leu	Ser															
			1825					1830					1835																	
GAC	GAG	TTC	TGC	CTG	GAC	GAG	AAG	AAG	GAG	CTG	AGC	GAG	AAG	GTG	AAG														2016	
Asp	Glu	Phe	Cys	Leu	Asp	Glu	Lys	Lys	Glu	Leu	Ser	Glu	Lys	Val	Lys															
			1840				1845						1850																	
CAC	GCC	AAG	CGC	CTG	AGC	GAC	GAG	CGC	AAC	CTG	CTG	CAG	GAC	CCC	AAC														2064	
His	Ala	Lys	Arg	Leu	Ser	Asp	Glu	Arg	Asn	Leu	Leu	Gln	Asp	Pro	Asn															
			1855				1860					1865																		
TTC	CGC	GGC	ATC	AAC	CGC	CAG	CTG	GAC	CGC	GGC	TGG	CGA	GGC	AGC	ACC														2112	
Phe	Arg	Gly	Ile	Asn	Arg	Gln	Leu	Asp	Arg	Gly	Trp	Arg	Gly	Ser	Thr															
			1870			1875					1880				1885															
GAT	ATC	ACC	ATC	CAG	GGC	GGC	GAC	GAC	GTG	TTC	AAG	GAG	AAC	TAC	GTG														2160	
Asp	Ile	Thr	Ile	Gln	Gly	Gly	Asp	Asp	Val	Phe	Lys	Glu	Asn	Tyr	Val															
				1890					1895					1900																
ACC	CTG	CTG	GGC	ACC	TTC	GAC	GAG	TGC	TAC	CCC	ACC	TAC	CTG	TAC	CAG														2208	
Thr	Leu	Leu	Gly	Thr	Phe	Asp	Glu	Cys	Tyr	Pro	Thr	Tyr	Leu	Tyr	Gln															
			1905					1910					1915																	
AAG	ATC	GAC	GAG	AGC	AAG	CTG	AAG	GCC	TAC	ACC	CGC	TAC	CAG	CTG	CGC														2256	
Lys	Ile	Asp	Glu	Ser	Lys	Leu	Lys	Ala	Tyr	Thr	Arg	Tyr	Gln	Leu	Arg															
			1920				1925						1930																	
GGC	TAC	ATC	GAG	GAC	AGC	CAG	GAC	CTG	GAA	ATC	TAC	CTG	ATC	CGC	TAC														2304	
Gly	Tyr	Ile	Glu	Asp	Ser	Gln	Asp	Leu	Glu	Ile	Tyr	Leu	Ile	Arg	Tyr															
			1935				1940					1945																		
AAC	GCC	AAG	CAC	GAG	ACC	GTG	AAC	GTG	CCC	GGC	ACC	GGC	AGC	CTG	TGG														2352	
Asn	Ala	Lys	His	Glu	Thr	Val	Asn	Val	Pro	Gly	Thr	Gly	Ser	Leu	Trp															
			1950			1955				1960					1965															
CCC	CTG	AGC	GCC	CCC	AGC	CCC	ATC	GGC	AAG	TGC	GGG	GAG	CCG	AAT	CGA														2400	
Pro	Leu	Ser	Ala	Pro	Ser	Pro	Ile	Gly	Lys	Cys	Gly	Glu	Pro	Asn	Arg															
				1970					1975					1980																

TGC GCT CCG CAC CTG GAG TGG AAC CCG GAC CTA GAC TGC AGC TGC AGG Cys Ala Pro His Leu Glu Trp Asn Pro Asp Leu Asp Cys Ser Cys Arg 1985 1990 1995	2448
GAC GGG GAG AAG TGC GCC CAC CAC AGC CAC CAC TTC AGC CTG GAC ATC Asp Gly Glu Lys Cys Ala His His Ser His His Phe Ser Leu Asp Ile 2000 2005 2010	2496
GAC GTG GGC TGC ACC GAC CTG AAC GAG GAC CTG GGC GTG TGG GTG ATC Asp Val Gly Cys Thr Asp Leu Asn Glu Asp Leu Gly Val Trp Val Ile 2015 2020 2025	2544
TTC AAG ATC AAG ACC CAG GAC GGC CAC GCC CGC CTG GGC AAT CTA GAA Phe Lys Ile Lys Thr Gln Asp Gly His Ala Arg Leu Gly Asn Leu Glu 2030 2035 2040 2045	2592
TTT CTC GAA GAG AAA CCA TTA GTA GGA GAA GCA CTA GCT CGT GTG AAA Phe Leu Glu Glu Lys Pro Leu Val Gly Glu Ala Leu Ala Arg Val Lys 2050 2055 2060	2640
AGA GCG GAG AAA AAA TGG AGA GAC AAA CGT GAA AAA TTG GAA TGG GAA Arg Ala Glu Lys Lys Trp Arg Asp Lys Arg Glu Lys Leu Glu Trp Glu 2065 2070 2075	2688
ACA AAT ATT GTT TAT AAA GAG GCA AAA GAA TCT GTA GAT GCT TTA TTT Thr Asn Ile Val Tyr Lys Glu Ala Lys Glu Ser Val Asp Ala Leu Phe 2080 2085 2090	2736
GTA AAC TCT CAA TAT GAT AGA TTA CAA GCG GAT ACC AAC ATC GCG ATG Val Asn Ser Gln Tyr Asp Arg Leu Gln Ala Asp Thr Asn Ile Ala Met 2095 2100 2105	2784
ATT CAT GCG GCA GAT AAA CGC GTT CAT AGC ATT CGA GAA GCT TAT CTG Ile His Ala Ala Asp Lys Arg Val His Ser Ile Arg Glu Ala Tyr Leu 2110 2115 2120 2125	2832
CCT GAG CTG TCT GTG ATT CCG GGT GTC AAT GCG GCT ATT TTT GAA GAA Pro Glu Leu Ser Val Ile Pro Gly Val Asn Ala Ala Ile Phe Glu Glu 2130 2135 2140	2880
TTA GAA GGG CGT ATT TTC ACT GCA TTC TCC CTA TAT GAT GCG AGA AAT Leu Glu Gly Arg Ile Phe Thr Ala Phe Ser Leu Tyr Asp Ala Arg Asn 2145 2150 2155	2928
GTC ATT AAA AAT GGT GAT TTT AAT AAT GGC TTA TCC TGC TGG AAC GTG Val Ile Lys Asn Gly Asp Phe Asn Asn Gly Leu Ser Cys Trp Asn Val 2160 2165 2170	2976
AAA GGG CAT GTA GAT GTA GAA GAA CAA AAC AAC CAC CGT TCG GTC CTT Lys Gly His Val Asp Val Glu Glu Gln Asn Asn His Arg Ser Val Leu 2175 2180 2185	3024
GTT GTT CCG GAA TGG GAA GCA GAA GTG TCA CAA GAA GTT CGT GTC TGT Val Val Pro Glu Trp Glu Ala Glu Val Ser Gln Glu Val Arg Val Cys 2190 2195 2200 2205	3072
CCG GGT CGT GGC TAT ATC CTT CGT GTC ACA GCG TAC AAG GAG GGA TAT Pro Gly Arg Gly Tyr Ile Leu Arg Val Thr Ala Tyr Lys Glu Gly Tyr 2210 2215 2220	3120

GGA GAA GGT TGC GTA ACC ATT CAT GAG ATC GAG AAC AAT ACA GAC GAA Gly Glu Gly Cys Val Thr Ile His Glu Ile Glu Asn Asn Thr Asp Glu 2225 2230 2235	3168
CTG AAG TTT AGC AAC TGT GTA GAA GAG GAA GTA TAT CCA AAC AAC ACG Leu Lys Phe Ser Asn Cys Val Glu Glu Glu Val Tyr Pro Asn Asn Thr 2240 2245 2250	3216
GTA ACG TGT AAT GAT TAT ACT GCG ACT CAA GAA GAA TAT GAG GGT ACG Val Thr Cys Asn Asp Tyr Thr Ala Thr Gln Glu Glu Tyr Glu Gly Thr 2255 2260 2265	3264
TAC ACT TCT CGT AAT CGA GGA TAT GAC GGA GCC TAT GAA AGC AAT TCT Tyr Thr Ser Arg Asn Arg Gly Tyr Asp Gly Ala Tyr Glu Ser Asn Ser 2270 2275 2280 2285	3312
TCT GTA CCA GCT GAT TAT GCA TCA GCC TAT GAA GAA AAA GCA TAT ACA Ser Val Pro Ala Asp Tyr Ala Ser Ala Tyr Glu Glu Lys Ala Tyr Thr 2290 2295 2300	3360
GAT GGA CGA AGA GAC AAT CCT TGT GAA TCT AAC AGA GGA TAT GGG GAT Asp Gly Arg Arg Asp Asn Pro Cys Glu Ser Asn Arg Gly Tyr Gly Asp 2305 2310 2315	3408
TAC ACA CCA CTA CCA GCT GGC TAT GTG ACA AAA GAA TTA GAG TAC TTC Tyr Thr Pro Leu Pro Ala Gly Tyr Val Thr Lys Glu Leu Glu Tyr Phe 2320 2325 2330	3456
CCA GAA ACC GAT AAG GTA TGG ATT GAG ATC GGA GAA ACG GAA GGA ACA Pro Glu Thr Asp Lys Val Trp Ile Glu Ile Gly Glu Thr Glu Gly Thr 2335 2340 2345	3504
TTC ATC GTG GAC AGC GTG GAA TTA CTT CTT ATG GAG GAA TAA Phe Ile Val Asp Ser Val Glu Leu Leu Leu Met Glu Glu 2350 2355 2360	3546

(2) INFORMATION FOR SEQ ID NO:13:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1181 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

Met Asp Asn Asn Pro Asn Ile Asn Glu Cys Ile Pro Tyr Asn Cys Leu 1 5 10 15
Ser Asn Pro Glu Val Glu Val Leu Gly Gly Glu Arg Ile Glu Thr Gly 20 25 30
Tyr Thr Pro Ile Asp Ile Ser Leu Ser Leu Thr Gln Phe Leu Leu Ser 35 40 45
Glu Phe Val Pro Gly Ala Gly Phe Val Leu Gly Leu Val Asp Ile Ile 50 55 60
Trp Gly Ile Phe Gly Pro Ser Gln Trp Asp Ala Phe Leu Val Gln Ile

65	70	75	80
Glu Gln Leu Ile Asn Gln Arg Ile Glu Glu Phe Ala Arg Asn Gln Ala	85	90	95
Ile Ser Arg Leu Glu Gly Leu Ser Asn Leu Tyr Gln Ile Tyr Ala Glu	100	105	110
Ser Phe Arg Glu Trp Glu Ala Asp Pro Thr Asn Pro Ala Leu Arg Glu	115	120	125
Glu Met Arg Ile Gln Phe Asn Asp Met Asn Ser Ala Leu Thr Thr Ala	130	135	140
Ile Pro Leu Phe Ala Val Gln Asn Tyr Gln Val Pro Leu Leu Ser Val	145	150	155
Tyr Val Gln Ala Ala Asn Leu His Leu Ser Val Leu Arg Asp Val Ser	165	170	175
Val Phe Gly Gln Arg Trp Gly Phe Asp Ala Ala Thr Ile Asn Ser Arg	180	185	190
Tyr Asn Asp Leu Thr Arg Leu Ile Gly Asn Tyr Thr Asp His Ala Val	195	200	205
Arg Trp Tyr Asn Thr Gly Leu Glu Arg Val Trp Gly Pro Asp Ser Arg	210	215	220
Asp Trp Ile Arg Tyr Asn Gln Phe Arg Arg Glu Leu Thr Leu Thr Val	225	230	235
Leu Asp Ile Val Ser Leu Phe Pro Asn Tyr Asp Ser Arg Thr Tyr Pro	245	250	255
Ile Arg Thr Val Ser Gln Leu Thr Arg Glu Ile Tyr Thr Asn Pro Val	260	265	270
Leu Glu Asn Phe Asp Gly Ser Phe Arg Gly Ser Ala Gln Gly Ile Glu	275	280	285
Gly Ser Ile Arg Ser Pro His Leu Met Asp Ile Leu Asn Ser Ile Thr	290	295	300
Ile Tyr Thr Asp Ala His Arg Gly Glu Tyr Tyr Trp Ser Gly His Gln	305	310	315
Ile Met Ala Ser Pro Val Gly Phe Ser Gly Pro Glu Phe Thr Phe Pro	325	330	335
Leu Tyr Gly Thr Met Gly Asn Ala Ala Pro Gln Gln Arg Ile Val Ala	340	345	350
Gln Leu Gly Gln Gly Val Tyr Arg Thr Leu Ser Ser Thr Leu Tyr Arg	355	360	365
Arg Pro Phe Asn Ile Gly Ile Asn Asn Gln Gln Leu Ser Val Leu Asp	370	375	380
Gly Thr Glu Phe Ala Tyr Gly Thr Ser Ser Asn Leu Pro Ser Ala Val	385	390	395
			400

Tyr	Arg	Lys	Ser	Gly	Thr	Val	Asp	Ser	Leu	Asp	Glu	Ile	Pro	Pro	Gln	
				405					410						415	
Asn	Asn	Asn	Val	Pro	Pro	Arg	Gln	Gly	Phe	Ser	His	Arg	Leu	Ser	His	
			420					425					430			
Val	Ser	Met	Phe	Arg	Ser	Gly	Phe	Ser	Asn	Ser	Ser	Val	Ser	Ile	Ile	
		435					440					445				
Arg	Ala	Pro	Met	Phe	Ser	Trp	Ile	His	Arg	Ser	Ala	Glu	Phe	Asn	Asn	
	450					455					460					
Ile	Ile	Pro	Ser	Ser	Gln	Ile	Thr	Gln	Ile	Pro	Leu	Thr	Lys	Ser	Thr	
465					470					475					480	
Asn	Leu	Gly	Ser	Gly	Thr	Ser	Val	Val	Lys	Gly	Pro	Gly	Phe	Thr	Gly	
				485					490					495		
Gly	Asp	Ile	Leu	Arg	Arg	Thr	Ser	Pro	Gly	Gln	Ile	Ser	Thr	Leu	Arg	
			500					505					510			
Val	Asn	Ile	Thr	Ala	Pro	Leu	Ser	Gln	Arg	Tyr	Arg	Val	Arg	Ile	Arg	
		515					520					525				
Tyr	Ala	Ser	Thr	Thr	Asn	Leu	Gln	Phe	His	Thr	Ser	Ile	Asp	Gly	Arg	
	530					535					540					
Pro	Ile	Asn	Gln	Gly	Asn	Phe	Ser	Ala	Thr	Met	Ser	Ser	Gly	Ser	Asn	
545					550					555					560	
Leu	Gln	Ser	Gly	Ser	Phe	Arg	Thr	Val	Gly	Phe	Thr	Thr	Pro	Phe	Asn	
				565					570					575		
Phe	Ser	Asn	Gly	Ser	Ser	Val	Phe	Thr	Leu	Ser	Ala	His	Val	Phe	Asn	
			580					585					590			
Ser	Gly	Asn	Glu	Val	Tyr	Ile	Asp	Arg	Ile	Glu	Phe	Val	Pro	Ala	Glu	
		595					600					605				
Val	Thr	Phe	Glu	Ala	Glu	Tyr	Asp	Leu	Glu	Arg	Ala	Gln	Lys	Ala	Val	
	610					615					620					
Asn	Glu	Leu	Phe	Thr	Ser	Ser	Asn	Gln	Ile	Gly	Leu	Lys	Thr	Asp	Val	
625					630					635					640	
Thr	Asp	Tyr	His	Ile	Asp	Gln	Val	Ser	Asn	Leu	Val	Glu	Cys	Leu	Ser	
				645					650					655		
Asp	Glu	Phe	Cys	Leu	Asp	Glu	Lys	Lys	Glu	Leu	Ser	Glu	Lys	Val	Lys	
			660					665					670			
His	Ala	Lys	Arg	Leu	Ser	Asp	Glu	Arg	Asn	Leu	Leu	Gln	Asp	Pro	Asn	
		675					680					685				
Phe	Arg	Gly	Ile	Asn	Arg	Gln	Leu	Asp	Arg	Gly	Trp	Arg	Gly	Ser	Thr	
	690					695					700					
Asp	Ile	Thr	Ile	Gln	Gly	Gly	Asp	Asp	Val	Phe	Lys	Glu	Asn	Tyr	Val	
705					710					715					720	

Thr	Leu	Leu	Gly	Thr	Phe	Asp	Glu	Cys	Tyr	Pro	Thr	Tyr	Leu	Tyr	Gln	725	730	735
Lys	Ile	Asp	Glu	Ser	Lys	Leu	Lys	Ala	Tyr	Thr	Arg	Tyr	Gln	Leu	Arg	740	745	750
Gly	Tyr	Ile	Glu	Asp	Ser	Gln	Asp	Leu	Glu	Ile	Tyr	Leu	Ile	Arg	Tyr	755	760	765
Asn	Ala	Lys	His	Glu	Thr	Val	Asn	Val	Pro	Gly	Thr	Gly	Ser	Leu	Trp	770	775	780
Pro	Leu	Ser	Ala	Pro	Ser	Pro	Ile	Gly	Lys	Cys	Gly	Glu	Pro	Asn	Arg	785	790	795
Cys	Ala	Pro	His	Leu	Glu	Trp	Asn	Pro	Asp	Leu	Asp	Cys	Ser	Cys	Arg	805	810	815
Asp	Gly	Glu	Lys	Cys	Ala	His	His	Ser	His	His	Phe	Ser	Leu	Asp	Ile	820	825	830
Asp	Val	Gly	Cys	Thr	Asp	Leu	Asn	Glu	Asp	Leu	Gly	Val	Trp	Val	Ile	835	840	845
Phe	Lys	Ile	Lys	Thr	Gln	Asp	Gly	His	Ala	Arg	Leu	Gly	Asn	Leu	Glu	850	855	860
Phe	Leu	Glu	Glu	Lys	Pro	Leu	Val	Gly	Glu	Ala	Leu	Ala	Arg	Val	Lys	865	870	875
Arg	Ala	Glu	Lys	Lys	Trp	Arg	Asp	Lys	Arg	Glu	Lys	Leu	Glu	Trp	Glu	885	890	895
Thr	Asn	Ile	Val	Tyr	Lys	Glu	Ala	Lys	Glu	Ser	Val	Asp	Ala	Leu	Phe	900	905	910
Val	Asn	Ser	Gln	Tyr	Asp	Arg	Leu	Gln	Ala	Asp	Thr	Asn	Ile	Ala	Met	915	920	925
Ile	His	Ala	Ala	Asp	Lys	Arg	Val	His	Ser	Ile	Arg	Glu	Ala	Tyr	Leu	930	935	940
Pro	Glu	Leu	Ser	Val	Ile	Pro	Gly	Val	Asn	Ala	Ala	Ile	Phe	Glu	Glu	945	950	955
Leu	Glu	Gly	Arg	Ile	Phe	Thr	Ala	Phe	Ser	Leu	Tyr	Asp	Ala	Arg	Asn	965	970	975
Val	Ile	Lys	Asn	Gly	Asp	Phe	Asn	Asn	Gly	Leu	Ser	Cys	Trp	Asn	Val	980	985	990
Lys	Gly	His	Val	Asp	Val	Glu	Glu	Gln	Asn	Asn	His	Arg	Ser	Val	Leu	995	1000	1005
Val	Val	Pro	Glu	Trp	Glu	Ala	Glu	Val	Ser	Gln	Glu	Val	Arg	Val	Cys	1010	1015	1020
Pro	Gly	Arg	Gly	Tyr	Ile	Leu	Arg	Val	Thr	Ala	Tyr	Lys	Glu	Gly	Tyr	1025	1030	1035
Gly	Glu	Gly	Cys	Val	Thr	Ile	His	Glu	Ile	Glu	Asn	Asn	Thr	Asp	Glu			

1045	1050	1055
Leu Lys Phe Ser Asn Cys Val Glu Glu Glu Val Tyr Pro Asn Asn Thr		
1060	1065	1070
Val Thr Cys Asn Asp Tyr Thr Ala Thr Gln Glu Glu Tyr Glu Gly Thr		
1075	1080	1085
Tyr Thr Ser Arg Asn Arg Gly Tyr Asp Gly Ala Tyr Glu Ser Asn Ser		
1090	1095	1100
Ser Val Pro Ala Asp Tyr Ala Ser Ala Tyr Glu Glu Lys Ala Tyr Thr		
1105	1110	1115
Asp Gly Arg Arg Asp Asn Pro Cys Glu Ser Asn Arg Gly Tyr Gly Asp		
1125	1130	1135
Tyr Thr Pro Leu Pro Ala Gly Tyr Val Thr Lys Glu Leu Glu Tyr Phe		
1140	1145	1150
Pro Glu Thr Asp Lys Val Trp Ile Glu Ile Gly Glu Thr Glu Gly Thr		
1155	1160	1165
Phe Ile Val Asp Ser Val Glu Leu Leu Leu Met Glu Glu		
1170	1175	1180

(2) INFORMATION FOR SEQ ID NO:14:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 3546 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: other nucleic acid
 - (A) DESCRIPTION: /desc = "Synthetic DNA"
- (iii) HYPOTHETICAL: NO
- (ix) FEATURE:
 - (A) NAME/KEY: CDS
 - (B) LOCATION: 1..3543
 - (D) OTHER INFORMATION: /product= "Full-length, hybrid, maize optimized heat stable cryIA(b)"
 - /note= "Disclosed in Figure 13 as contained in pCIB5513."

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

ATG GAC AAC AAC CCC AAC ATC AAC GAG TGC ATC CCC TAC AAC TGC CTG	48
Met Asp Asn Asn Pro Asn Ile Asn Glu Cys Ile Pro Tyr Asn Cys Leu	
1185	1190
AGC AAC CCC GAG GTG GAG GTG CTG GGC GGC GAG CGC ATC GAG ACC GGC	96
Ser Asn Pro Glu Val Glu Val Leu Gly Gly Glu Arg Ile Glu Thr Gly	
1200	1205
TAC ACC CCC ATC GAC ATC AGC CTG AGC CTG ACC CAG TTC CTG CTG AGC	144
Tyr Thr Pro Ile Asp Ile Ser Leu Ser Leu Thr Gln Phe Leu Leu Ser	
1215	1220

GAG TTC GTG CCC GGC GCC GGC TTC GTG CTG GGC CTG GTG GAC ATC ATC Glu Phe Val Pro Gly Ala Gly Phe Val Leu Gly Leu Val Asp Ile Ile 1230 1235 1240 1245	192
TGG GGC ATC TTC GGC CCC AGC CAG TGG GAC GCC TTC CTG GTG CAG ATC Trp Gly Ile Phe Gly Pro Ser Gln Trp Asp Ala Phe Leu Val Gln Ile 1250 1255 1260	240
GAG CAG CTG ATC AAC CAG CGC ATC GAG GAG TTC GCC CGC AAC CAG GCC Glu Gln Leu Ile Asn Gln Arg Ile Glu Glu Phe Ala Arg Asn Gln Ala 1265 1270 1275	288
ATC AGC CGC CTG GAG GGC CTG AGC AAC CTG TAC CAA ATC TAC GCC GAG Ile Ser Arg Leu Glu Gly Leu Ser Asn Leu Tyr Gln Ile Tyr Ala Glu 1280 1285 1290	336
AGC TTC CGC GAG TGG GAG GCC GAC CCC ACC AAC CCC GCC CTG CGC GAG Ser Phe Arg Glu Trp Glu Ala Asp Pro Thr Asn Pro Ala Leu Arg Glu 1295 1300 1305	384
GAG ATG CGC ATC CAG TTC AAC GAC ATG AAC AGC GCC CTG ACC ACC GCC Glu Met Arg Ile Gln Phe Asn Asp Met Asn Ser Ala Leu Thr Thr Ala 1310 1315 1320 1325	432
ATC CCC CTG TTC GCC GTG CAG AAC TAC CAG GTG CCC CTG CTG AGC GTG Ile Pro Leu Phe Ala Val Gln Asn Tyr Gln Val Pro Leu Leu Ser Val 1330 1335 1340	480
TAC GTG CAG GCC GCC AAC CTG CAC CTG AGC GTG CTG CGC GAC GTC AGC Tyr Val Gln Ala Ala Asn Leu His Leu Ser Val Leu Arg Asp Val Ser 1345 1350 1355	528
GTG TTC GGC CAG CGC TGG GGC TTC GAC GCC GCC ACC ATC AAC AGC CGC Val Phe Gly Gln Arg Trp Gly Phe Asp Ala Ala Thr Ile Asn Ser Arg 1360 1365 1370	576
TAC AAC GAC CTG ACC CGC CTG ATC GGC AAC TAC ACC GAC CAC GCC GTG Tyr Asn Asp Leu Thr Arg Leu Ile Gly Asn Tyr Thr Asp His Ala Val 1375 1380 1385	624
CGC TGG TAC AAC ACC GGC CTG GAG CGC GTG TGG GGT CCC GAC AGC CGC Arg Trp Tyr Asn Thr Gly Leu Glu Arg Val Trp Gly Pro Asp Ser Arg 1390 1395 1400 1405	672
GAC TGG ATC AGG TAC AAC CAG TTC CGC CGC GAG CTG ACC CTG ACC GTG Asp Trp Ile Arg Tyr Asn Gln Phe Arg Arg Glu Leu Thr Leu Thr Val 1410 1415 1420	720
CTG GAC ATC GTG AGC CTG TTC CCC AAC TAC GAC AGC CGC ACC TAC CCC Leu Asp Ile Val Ser Leu Phe Pro Asn Tyr Asp Ser Arg Thr Tyr Pro 1425 1430 1435	768
ATC CGC ACC GTG AGC CAG CTG ACC CGC GAG ATT TAC ACC AAC CCC GTG Ile Arg Thr Val Ser Gln Leu Thr Arg Glu Ile Tyr Thr Asn Pro Val 1440 1445 1450	816
CTG GAG AAC TTC GAC GGC AGC TTC CGC GGC AGC GCC CAG GGC ATC GAG Leu Glu Asn Phe Asp Gly Ser Phe Arg Gly Ser Ala Gln Gly Ile Glu 1455 1460 1465	864

GGC AGC ATC CGC AGC CCC CAC CTG ATG GAC ATC CTG AAC AGC ATC ACC Gly Ser Ile Arg Ser Pro His Leu Met Asp Ile Leu Asn Ser Ile Thr 1470 1475 1480 1485	912
ATC TAC ACC GAC GCC CAC CGC GGC GAG TAC TAC TGG AGC GGC CAC CAG Ile Tyr Thr Asp Ala His Arg Gly Glu Tyr Tyr Trp Ser Gly His Gln 1490 1495 1500	960
ATC ATG GCC AGC CCC GTC GGC TTC AGC GGC CCC GAG TTC ACC TTC CCC Ile Met Ala Ser Pro Val Gly Phe Ser Gly Pro Glu Phe Thr Phe Pro 1505 1510 1515	1008
CTG TAC GGC ACC ATG GGC AAC GCT GCA CCT CAG CAG CGC ATC GTG GCA Leu Tyr Gly Thr Met Gly Asn Ala Ala Pro Gln Gln Arg Ile Val Ala 1520 1525 1530	1056
CAG CTG GGC CAG GGA GTG TAC CGC ACC CTG AGC AGC ACC CTG TAC CGT Gln Leu Gly Gln Gly Val Tyr Arg Thr Leu Ser Ser Thr Leu Tyr Arg 1535 1540 1545	1104
CGA CCT TTC AAC ATC GGC ATC AAC AAC CAG CAG CTG AGC GTG CTG GAC Arg Pro Phe Asn Ile Gly Ile Asn Asn Gln Gln Leu Ser Val Leu Asp 1550 1555 1560 1565	1152
GGC ACC GAG TTC GCC TAC GGC ACC AGC AGC AAC CTG CCC AGC GCC GTG Gly Thr Glu Phe Ala Tyr Gly Thr Ser Ser Asn Leu Pro Ser Ala Val 1570 1575 1580	1200
TAC CGC AAG AGC GGC ACC GTG GAC AGC CTG GAC GAG ATC CCC CCT CAG Tyr Arg Lys Ser Gly Thr Val Asp Ser Leu Asp Glu Ile Pro Pro Gln 1585 1590 1595	1248
AAC AAC AAC GTG CCA CCT CGA CAG GGC TTC AGC CAC CGT CTG AGC CAC Asn Asn Asn Val Pro Pro Arg Gln Gly Phe Ser His Arg Leu Ser His 1600 1605 1610	1296
GTG AGC ATG TTC CGC AGT GGC TTC AGC AAC AGC AGC GTG AGC ATC ATC Val Ser Met Phe Arg Ser Gly Phe Ser Asn Ser Ser Val Ser Ile Ile 1615 1620 1625	1344
CGT GCA CCT ATG TTC AGC TGG ATT CAC CGC AGT GCC GAG TTC AAC AAC Arg Ala Pro Met Phe Ser Trp Ile His Arg Ser Ala Glu Phe Asn Asn 1630 1635 1640 1645	1392
ATC ATC CCC AGC AGC CAG ATC ACC CAG ATC CCC CTG ACC AAG AGC ACC Ile Ile Pro Ser Ser Gln Ile Thr Gln Ile Pro Leu Thr Lys Ser Thr 1650 1655 1660	1440
AAC CTG GGC AGC GGC ACC AGC GTG GTG AAG GGC CCC GGC TTC ACC GGC Asn Leu Gly Ser Gly Thr Ser Val Val Lys Gly Pro Gly Phe Thr Gly 1665 1670 1675	1488
GGC GAC ATC CTG CGC CGC ACC AGC CCC GGC CAG ATC AGC ACC CTG CGC Gly Asp Ile Leu Arg Arg Thr Ser Pro Gly Gln Ile Ser Thr Leu Arg 1680 1685 1690	1536
GTG AAC ATC ACC GCC CCC CTG AGC CAG CGC TAC CGC GTC CGC ATC CGC Val Asn Ile Thr Ala Pro Leu Ser Gln Arg Tyr Arg Val Arg Ile Arg 1695 1700 1705	1584
TAC GCC AGC ACC ACC AAC CTG CAG TTC CAC ACC AGC ATC GAC GGC CGC	1632

Tyr Ala Ser Thr Thr	Asn Leu Gln Phe His Thr Ser Ile Asp Gly Arg	1710	1715	1720	1725
CCC ATC AAC CAG GGC AAC TTC AGC GCC ACC ATG AGC AGC GGC AGC AAC	Pro Ile Asn Gln Gly Asn Phe Ser Ala Thr Met Ser Ser Gly Ser Asn	1680	1730	1735	1740
CTG CAG AGC GGC AGC TTC CGC ACC GTG GGC TTC ACC ACC CCC TTC AAC	Leu Gln Ser Gly Ser Phe Arg Thr Val Gly Phe Thr Thr Pro Phe Asn	1728	1745	1750	1755
TTC AGC AAC GGC AGC AGC GTG TTC ACC CTG AGC GCC CAC GTG TTC AAC	Phe Ser Asn Gly Ser Ser Val Phe Thr Leu Ser Ala His Val Phe Asn	1776	1760	1765	1770
AGC GGC AAC GAG GTG TAC ATC GAC CGC ATC GAG TTC GTG CCC GCC GAG	Ser Gly Asn Glu Val Tyr Ile Asp Arg Ile Glu Phe Val Pro Ala Glu	1824	1775	1780	1785
GTG ACC TTC GAG GCC GAG TAC GAC CTG GAG AGG GCT CAG AAG GCC GTG	Val Thr Phe Glu Ala Glu Tyr Asp Leu Glu Arg Ala Gln Lys Ala Val	1872	1790	1795	1800
AAC GAG CTG TTC ACC AGC AGC AAC CAG ATC GGC CTG AAG ACC GAC GTG	Asn Glu Leu Phe Thr Ser Ser Asn Gln Ile Gly Leu Lys Thr Asp Val	1920	1810	1815	1820
ACC GAC TAC CAC ATC GAC CAG GTG AGC AAC CTG GTG GAG TGC TTA AGC	Thr Asp Tyr His Ile Asp Gln Val Ser Asn Leu Val Glu Cys Leu Ser	1968	1825	1830	1835
GAC GAG TTC TGC CTG GAC GAG AAG AAG GAG CTG AGC GAG AAG GTG AAG	Asp Glu Phe Cys Leu Asp Glu Lys Lys Glu Leu Ser Glu Lys Val Lys	2016	1840	1845	1850
CAC GCC AAG CGC CTG AGC GAC GAG CGC AAC CTG CTG CAG GAC CCC AAC	His Ala Lys Arg Leu Ser Asp Glu Arg Asn Leu Leu Gln Asp Pro Asn	2064	1855	1860	1865
TTC CGC GGC ATC AAC CGC CAG CTG GAC CGC GGC TGG CGA GGC AGC ACC	Phe Arg Gly Ile Asn Arg Gln Leu Asp Arg Gly Trp Arg Gly Ser Thr	2112	1870	1875	1880
GAT ATC ACC ATC CAG GGC GGC GAC GAC GTG TTC AAG GAG AAC TAC GTG	Asp Ile Thr Ile Gln Gly Gly Asp Asp Val Phe Lys Glu Asn Tyr Val	2160	1890	1895	1900
ACC CTG CAG GGC ACC TTC GAC GAG TGC TAC CCC ACC TAC CTG TAC CAG	Thr Leu Gln Gly Thr Phe Asp Glu Cys Tyr Pro Thr Tyr Leu Tyr Gln	2208	1905	1910	1915
CCG ATC GAC GAG AGC AAG CTG AAG GCC TAC ACC CGC TAC CAG CTG CGC	Pro Ile Asp Glu Ser Lys Leu Lys Ala Tyr Thr Arg Tyr Gln Leu Arg	2256	1920	1925	1930
GGC TAC ATC GAG GAC AGC CAG GAC CTG GAA ATC TAC CTG ATC CGC TAC	Gly Tyr Ile Glu Asp Ser Gln Asp Leu Glu Ile Tyr Leu Ile Arg Tyr	2304	1935	1940	1945
AAC GCC AAG CAC GAG ACC GTG AAC GTG CCC GGC ACC GGC AGC CTG TGG	Asn Ala Lys His Glu Thr Val Asn Val Pro Gly Thr Gly Ser Leu Trp	2352			

1950				1955				1960				1965					
CCC Pro	CTG Leu	AGC Ser	GCC Ala	CCC Pro	AGC Ser	CCC Pro	ATC Ile	GGC Gly	AAG Lys	TGC Cys	GGG Gly	GAG Glu	CCG Pro	AAT Asn	CGA Arg	2400	
				1970				1975				1980					
TGC Cys	GCT Ala	CCG Pro	CAC His	CTG Leu	GAG Glu	TGG Trp	AAC Asn	CCG Pro	GAC Asp	CTA Leu	GAC Asp	TGC Cys	AGC Ser	TGC Cys	AGG Arg	2448	
				1985				1990				1995					
GAC Asp	GGG Gly	GAG Glu	AAG Lys	TGC Cys	GCC Ala	CAC His	CAC His	AGC Ser	CAC His	CAC His	TTC Phe	AGC Ser	CTG Leu	GAC Asp	ATC Ile	2496	
				2000				2005				2010					
GAC Asp	GTG Val	GGC Gly	TGC Cys	ACC Thr	GAC Asp	CTG Leu	AAC Asn	GAG Glu	GAC Asp	CTG Leu	GGC Gly	GTG Val	TGG Trp	GTG Val	ATC Ile	2544	
				2015				2020				2025					
TTC Phe	AAG Lys	ATC Ile	AAG Lys	ACC Thr	CAG Gln	GAC Asp	GGC Gly	CAC His	GCC Ala	CGC Arg	CTG Leu	GGC Gly	AAT Asn	CTA Leu	GAG Glu	2592	
				2030				2035				2040				2045	
TTC Phe	CTG Leu	GAG Glu	GAG Glu	AAG Lys	CCC Pro	CTG Leu	GTG Val	GGC Gly	GAG Glu	GCC Ala	CTG Leu	GCC Ala	CGC Arg	GTG Val	AAG Lys	2640	
				2050				2055				2060					
CGC Arg	GCC Ala	GAG Glu	AAG Lys	AAG Lys	TGG Trp	CGC Arg	GAC Asp	AAG Lys	CGC Arg	GAG Glu	AAG Lys	CTG Leu	GAG Glu	TGG Trp	GAG Glu	2688	
				2065				2070				2075					
ACC Thr	AAC Asn	ATC Ile	GTG Val	TAC Tyr	AAG Lys	GAG Glu	GCC Ala	AAG Lys	GAG Glu	AGC Ser	GTG Val	GAC Asp	GCC Ala	CTG Leu	TTC Phe	2736	
				2080				2085				2090					
GTG Val	AAC Asn	AGC Ser	CAG Gln	TAC Tyr	GAC Asp	CGC Arg	CTG Leu	CAG Gln	GCC Ala	GAC Asp	ACC Thr	AAC Asn	ATC Ile	GCC Ala	ATG Met	2784	
				2095				2100				2105					
ATC Ile	CAC His	GCC Ala	GCC Ala	GAC Asp	AAG Lys	CGC Arg	GTG Val	CAC His	AGC Ser	ATT Ile	CGC Arg	GAG Glu	GCC Ala	TAC Tyr	CTG Leu	2832	
				2110				2115				2120				2125	
CCC Pro	GAG Glu	CTG Leu	AGC Ser	GTG Val	ATC Ile	CCC Pro	GGC Gly	GTG Val	AAC Asn	GCC Ala	GCC Ala	ATC Ile	TTC Phe	GAG Glu	GAA Glu	2880	
				2130				2135				2140					
CTC Leu	GAG Glu	GGC Gly	CGC Arg	ATC Ile	TTC Phe	ACC Thr	GCC Ala	TTC Phe	AGC Ser	CTG Leu	TAC Tyr	GAC Asp	GCC Ala	CGC Arg	AAC Asn	2928	
				2145				2150				2155					
GTG Val	ATC Ile	AAG Lys	AAC Asn	GGC Gly	GAC Asp	TTC Phe	AAC Asn	AAC Asn	GGC Gly	CTG Leu	AGC Ser	TGC Cys	TGG Trp	AAC Asn	GTG Val	2976	
				2160				2165				2170					
AAG Lys	GGC Gly	CAC His	GTG Val	GAC Asp	GTG Val	GAG Glu	GAG Glu	CAG Gln	AAC Asn	AAC Asn	CAC His	CGC Arg	AGC Ser	GTG Val	CTG Leu	3024	
				2175				2180				2185					
GTG Val	GTG Val	CCC Pro	GAG Glu	TGG Trp	GAG Glu	GCC Ala	GAG Glu	GTG Val	AGC Ser	CAG Gln	GAG Glu	GTG Val	CGC Arg	GTG Val	TGC Cys	3072	
				2190				2195				2200				2205	

CCC GGC CGC GGC TAC ATC CTG CGC GTG ACC GCC TAC AAG GAG GGC TAC Pro Gly Arg Gly Tyr Ile Leu Arg Val Thr Ala Tyr Lys Glu Gly Tyr 2210 2215 2220	3120
GGC GAG GGC TGC GTG ACC ATC CAC GAG ATC GAG AAC AAC ACC GAC GAG Gly Glu Gly Cys Val Thr Ile His Glu Ile Glu Asn Asn Thr Asp Glu 2225 2230 2235	3168
CTC AAG TTC AGC AAC TGC GTG GAG GAG GAG GTT TAC CCC AAC AAC ACC Leu Lys Phe Ser Asn Cys Val Glu Glu Glu Val Tyr Pro Asn Asn Thr 2240 2245 2250	3216
GTG ACC TGC AAC GAC TAC ACC GCG ACC CAG GAG GAG TAC GAA GGC ACC Val Thr Cys Asn Asp Tyr Thr Ala Thr Gln Glu Glu Tyr Glu Gly Thr 2255 2260 2265	3264
TAC ACC TCT CGC AAC AGG GGT TAC GAC GGC GCC TAC GAG TCC AAC AGC Tyr Thr Ser Arg Asn Arg Gly Tyr Asp Gly Ala Tyr Glu Ser Asn Ser 2270 2275 2280 2285	3312
TCC GTG CCA GCC GAC TAC GCC AGC GCC TAC GAG GAG AAA GCC TAC ACC Ser Val Pro Ala Asp Tyr Ala Ser Ala Tyr Glu Glu Lys Ala Tyr Thr 2290 2295 2300	3360
GAC GGT AGA CGC GAC AAC CCA TGT GAG AGC AAC AGA GGC TAC GGC GAC Asp Gly Arg Arg Asp Asn Pro Cys Glu Ser Asn Arg Gly Tyr Gly Asp 2305 2310 2315	3408
TAC ACC CCC CTG CCC GCT GGA TAC GTG ACC AAG GAG CTG GAG TAC TTC Tyr Thr Pro Leu Pro Ala Gly Tyr Val Thr Lys Glu Leu Glu Tyr Phe 2320 2325 2330	3456
CCC GAG ACC GAC AAG GTG TGG ATC GAG ATT GGC GAG ACC GAG GGC ACC Pro Glu Thr Asp Lys Val Trp Ile Glu Ile Gly Glu Thr Glu Gly Thr 2335 2340 2345	3504
TTC ATC GTG GAC AGC GTG GAG CTG CTG CTG ATG GAG GAG TAG Phe Ile Val Asp Ser Val Glu Leu Leu Leu Met Glu Glu 2350 2355 2360	3546

(2) INFORMATION FOR SEQ ID NO:15:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1181 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

Met	Asp	Asn	Asn	Pro	Asn	Ile	Asn	Glu	Cys	Ile	Pro	Tyr	Asn	Cys	Leu
1				5				10						15	
Ser	Asn	Pro	Glu	Val	Glu	Val	Leu	Gly	Gly	Glu	Arg	Ile	Glu	Thr	Gly
			20					25					30		
Tyr	Thr	Pro	Ile	Asp	Ile	Ser	Leu	Ser	Leu	Thr	Gln	Phe	Leu	Leu	Ser
		35					40					45			

Glu Phe Val Pro Gly Ala Gly Phe Val Leu Gly Leu Val Asp Ile Ile
 50 55 60
 Trp Gly Ile Phe Gly Pro Ser Gln Trp Asp Ala Phe Leu Val Gln Ile
 65 70 75 80
 Glu Gln Leu Ile Asn Gln Arg Ile Glu Glu Phe Ala Arg Asn Gln Ala
 85 90 95
 Ile Ser Arg Leu Glu Gly Leu Ser Asn Leu Tyr Gln Ile Tyr Ala Glu
 100 105 110
 Ser Phe Arg Glu Trp Glu Ala Asp Pro Thr Asn Pro Ala Leu Arg Glu
 115 120 125
 Glu Met Arg Ile Gln Phe Asn Asp Met Asn Ser Ala Leu Thr Thr Ala
 130 135 140
 Ile Pro Leu Phe Ala Val Gln Asn Tyr Gln Val Pro Leu Leu Ser Val
 145 150 155 160
 Tyr Val Gln Ala Ala Asn Leu His Leu Ser Val Leu Arg Asp Val Ser
 165 170 175
 Val Phe Gly Gln Arg Trp Gly Phe Asp Ala Ala Thr Ile Asn Ser Arg
 180 185 190
 Tyr Asn Asp Leu Thr Arg Leu Ile Gly Asn Tyr Thr Asp His Ala Val
 195 200 205
 Arg Trp Tyr Asn Thr Gly Leu Glu Arg Val Trp Gly Pro Asp Ser Arg
 210 215 220
 Asp Trp Ile Arg Tyr Asn Gln Phe Arg Arg Glu Leu Thr Leu Thr Val
 225 230 235 240
 Leu Asp Ile Val Ser Leu Phe Pro Asn Tyr Asp Ser Arg Thr Tyr Pro
 245 250 255
 Ile Arg Thr Val Ser Gln Leu Thr Arg Glu Ile Tyr Thr Asn Pro Val
 260 265 270
 Leu Glu Asn Phe Asp Gly Ser Phe Arg Gly Ser Ala Gln Gly Ile Glu
 275 280 285
 Gly Ser Ile Arg Ser Pro His Leu Met Asp Ile Leu Asn Ser Ile Thr
 290 295 300
 Ile Tyr Thr Asp Ala His Arg Gly Glu Tyr Tyr Trp Ser Gly His Gln
 305 310 315 320
 Ile Met Ala Ser Pro Val Gly Phe Ser Gly Pro Glu Phe Thr Phe Pro
 325 330 335
 Leu Tyr Gly Thr Met Gly Asn Ala Ala Pro Gln Gln Arg Ile Val Ala
 340 345 350
 Gln Leu Gly Gln Gly Val Tyr Arg Thr Leu Ser Ser Thr Leu Tyr Arg
 355 360 365

Arg Pro Phe Asn Ile Gly Ile Asn Asn Gln Gln Leu Ser Val Leu Asp
370 375 380

Gly Thr Glu Phe Ala Tyr Gly Thr Ser Ser Asn Leu Pro Ser Ala Val
385 390 395 400

Tyr Arg Lys Ser Gly Thr Val Asp Ser Leu Asp Glu Ile Pro Pro Gln
405 410 415

Asn Asn Asn Val Pro Pro Arg Gln Gly Phe Ser His Arg Leu Ser His
420 425 430

Val Ser Met Phe Arg Ser Gly Phe Ser Asn Ser Ser Val Ser Ile Ile
435 440 445

Arg Ala Pro Met Phe Ser Trp Ile His Arg Ser Ala Glu Phe Asn Asn
450 455 460

Ile Ile Pro Ser Ser Gln Ile Thr Gln Ile Pro Leu Thr Lys Ser Thr
465 470 475 480

Asn Leu Gly Ser Gly Thr Ser Val Val Lys Gly Pro Gly Phe Thr Gly
485 490 495

Gly Asp Ile Leu Arg Arg Thr Ser Pro Gly Gln Ile Ser Thr Leu Arg
500 505 510

Val Asn Ile Thr Ala Pro Leu Ser Gln Arg Tyr Arg Val Arg Ile Arg
515 520 525

Tyr Ala Ser Thr Thr Asn Leu Gln Phe His Thr Ser Ile Asp Gly Arg
530 535 540

Pro Ile Asn Gln Gly Asn Phe Ser Ala Thr Met Ser Ser Gly Ser Asn
545 550 555 560

Leu Gln Ser Gly Ser Phe Arg Thr Val Gly Phe Thr Thr Pro Phe Asn
565 570 575

Phe Ser Asn Gly Ser Ser Val Phe Thr Leu Ser Ala His Val Phe Asn
580 585 590

Ser Gly Asn Glu Val Tyr Ile Asp Arg Ile Glu Phe Val Pro Ala Glu
595 600 605

Val Thr Phe Glu Ala Glu Tyr Asp Leu Glu Arg Ala Gln Lys Ala Val
610 615 620

Asn Glu Leu Phe Thr Ser Ser Asn Gln Ile Gly Leu Lys Thr Asp Val
625 630 635 640

Thr Asp Tyr His Ile Asp Gln Val Ser Asn Leu Val Glu Cys Leu Ser
645 650 655

Asp Glu Phe Cys Leu Asp Glu Lys Lys Glu Leu Ser Glu Lys Val Lys
660 665 670

His Ala Lys Arg Leu Ser Asp Glu Arg Asn Leu Leu Gln Asp Pro Asn
675 680 685

Phe Arg Gly Ile Asn Arg Gln Leu Asp Arg Gly Trp Arg Gly Ser Thr

690				695				700							
Asp 705	Ile	Thr	Ile	Gln	Gly 710	Gly	Asp	Asp	Val	Phe 715	Lys	Glu	Asn	Tyr	Val 720
Thr	Leu	Gln	Gly	Thr 725	Phe	Asp	Glu	Cys	Tyr 730	Pro	Thr	Tyr	Leu	Tyr 735	Gln
Pro	Ile	Asp	Glu 740	Ser	Lys	Leu	Lys	Ala 745	Tyr	Thr	Arg	Tyr	Gln 750	Leu	Arg
Gly	Tyr	Ile 755	Glu	Asp	Ser	Gln	Asp 760	Leu	Glu	Ile	Tyr	Leu 765	Ile	Arg	Tyr
Asn 770	Ala	Lys	His	Glu	Thr	Val 775	Asn	Val	Pro	Gly	Thr 780	Gly	Ser	Leu	Trp
Pro 785	Leu	Ser	Ala	Pro	Ser 790	Pro	Ile	Gly	Lys	Cys 795	Gly	Glu	Pro	Asn	Arg 800
Cys	Ala	Pro	His	Leu 805	Glu	Trp	Asn	Pro	Asp 810	Leu	Asp	Cys	Ser	Cys 815	Arg
Asp	Gly	Glu	Lys 820	Cys	Ala	His	His	Ser 825	His	His	Phe	Ser	Leu 830	Asp	Ile
Asp	Val	Gly 835	Cys	Thr	Asp	Leu	Asn 840	Glu	Asp	Leu	Gly	Val 845	Trp	Val	Ile
Phe 850	Lys	Ile	Lys	Thr	Gln	Asp 855	Gly	His	Ala	Arg	Leu 860	Gly	Asn	Leu	Glu
Phe 865	Leu	Glu	Glu	Lys	Pro 870	Leu	Val	Gly	Glu	Ala 875	Leu	Ala	Arg	Val	Lys 880
Arg	Ala	Glu	Lys	Lys 885	Trp	Arg	Asp	Lys	Arg 890	Glu	Lys	Leu	Glu	Trp 895	Glu
Thr	Asn	Ile	Val 900	Tyr	Lys	Glu	Ala	Lys 905	Glu	Ser	Val	Asp	Ala 910	Leu	Phe
Val	Asn	Ser 915	Gln	Tyr	Asp	Arg	Leu 920	Gln	Ala	Asp	Thr	Asn 925	Ile	Ala	Met
Ile 930	His	Ala	Ala	Asp	Lys	Arg 935	Val	His	Ser	Ile	Arg 940	Glu	Ala	Tyr	Leu
Pro 945	Glu	Leu	Ser	Val	Ile 950	Pro	Gly	Val	Asn	Ala 955	Ala	Ile	Phe	Glu	Glu 960
Leu	Glu	Gly	Arg	Ile 965	Phe	Thr	Ala	Phe	Ser 970	Leu	Tyr	Asp	Ala	Arg 975	Asn
Val	Ile	Lys	Asn 980	Gly	Asp	Phe	Asn	Asn 985	Gly	Leu	Ser	Cys	Trp 990	Asn	Val
Lys	Gly	His 995	Val	Asp	Val	Glu	Glu 1000	Gln	Asn	Asn	His	Arg	Ser	Val	Leu
Val	Val 1010	Pro	Glu	Trp	Glu	Ala 1015	Glu	Val	Ser	Gln	Glu 1020	Val	Arg	Val	Cys

Pro Gly Arg Gly Tyr Ile Leu Arg Val Thr Ala Tyr Lys Glu Gly Tyr
1025 1030 1035 1040

Gly Glu Gly Cys Val Thr Ile His Glu Ile Glu Asn Asn Thr Asp Glu
1045 1050 1055

Leu Lys Phe Ser Asn Cys Val Glu Glu Glu Val Tyr Pro Asn Asn Thr
1060 1065 1070

Val Thr Cys Asn Asp Tyr Thr Ala Thr Gln Glu Glu Tyr Glu Gly Thr
1075 1080 1085

Tyr Thr Ser Arg Asn Arg Gly Tyr Asp Gly Ala Tyr Glu Ser Asn Ser
1090 1095 1100

Ser Val Pro Ala Asp Tyr Ala Ser Ala Tyr Glu Glu Lys Ala Tyr Thr
1105 1110 1115 1120

Asp Gly Arg Arg Asp Asn Pro Cys Glu Ser Asn Arg Gly Tyr Gly Asp
1125 1130 1135

Tyr Thr Pro Leu Pro Ala Gly Tyr Val Thr Lys Glu Leu Glu Tyr Phe
1140 1145 1150

Pro Glu Thr Asp Lys Val Trp Ile Glu Ile Gly Glu Thr Glu Gly Thr
1155 1160 1165

Phe Ile Val Asp Ser Val Glu Leu Leu Leu Met Glu Glu
1170 1175 1180

(2) INFORMATION FOR SEQ ID NO:16:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 3547 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

- (A) DESCRIPTION: /desc = "Synthetic DNA"

(iii) HYPOTHETICAL: NO

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1..3543
- (D) OTHER INFORMATION: /product= "Full-length, hybrid, maize optimized heat stable cryIA(b)"
- /note= "Disclosed in Figure 15 as contained in pCIB5514."

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

ATG GAC AAC AAC CCC AAC ATC AAC GAG TGC ATC CCC TAC AAC TGC CTG 48
Met Asp Asn Asn Pro Asn Ile Asn Glu Cys Ile Pro Tyr Asn Cys Leu
1185 1190 1195

AGC AAC CCC GAG GTG GAG GTG CTG GGC GGC GAG CGC ATC GAG ACC GGC 96
Ser Asn Pro Glu Val Glu Val Leu Gly Gly Glu Arg Ile Glu Thr Gly

1200	1205	1210	
TAC ACC CCC ATC GAC ATC AGC CTG AGC CTG ACC CAG TTC CTG CTG AGC Tyr Thr Pro Ile Asp Ile Ser Leu Ser Leu Thr Gln Phe Leu Leu Ser 1215 1220 1225			144
GAG TTC GTG CCC GGC GCC GGC TTC GTG CTG GGC CTG GTG GAC ATC ATC Glu Phe Val Pro Gly Ala Gly Phe Val Leu Gly Leu Val Asp Ile Ile 1230 1235 1240 1245			192
TGG GGC ATC TTC GGC CCC AGC CAG TGG GAC GCC TTC CTG GTG CAG ATC Trp Gly Ile Phe Gly Pro Ser Gln Trp Asp Ala Phe Leu Val Gln Ile 1250 1255 1260			240
GAG CAG CTG ATC AAC CAG CGC ATC GAG GAG TTC GCC CGC AAC CAG GCC Glu Gln Leu Ile Asn Gln Arg Ile Glu Glu Phe Ala Arg Asn Gln Ala 1265 1270 1275			288
ATC AGC CGC CTG GAG GGC CTG AGC AAC CTG TAC CAA ATC TAC GCC GAG Ile Ser Arg Leu Glu Gly Leu Ser Asn Leu Tyr Gln Ile Tyr Ala Glu 1280 1285 1290			336
AGC TTC CGC GAG TGG GAG GCC GAC CCC ACC AAC CCC GCC CTG CGC GAG Ser Phe Arg Glu Trp Glu Ala Asp Pro Thr Asn Pro Ala Leu Arg Glu 1295 1300 1305			384
GAG ATG CGC ATC CAG TTC AAC GAC ATG AAC AGC GCC CTG ACC ACC GCC Glu Met Arg Ile Gln Phe Asn Asp Met Asn Ser Ala Leu Thr Thr Ala 1310 1315 1320 1325			432
ATC CCC CTG TTC GCC GTG CAG AAC TAC CAG GTG CCC CTG CTG AGC GTG Ile Pro Leu Phe Ala Val Gln Asn Tyr Gln Val Pro Leu Leu Ser Val 1330 1335 1340			480
TAC GTG CAG GCC GCC AAC CTG CAC CTG AGC GTG CTG CGC GAC GTC AGC Tyr Val Gln Ala Ala Asn Leu His Leu Ser Val Leu Arg Asp Val Ser 1345 1350 1355			528
GTG TTC GGC CAG CGC TGG GGC TTC GAC GCC GCC ACC ATC AAC AGC CGC Val Phe Gly Gln Arg Trp Gly Phe Asp Ala Ala Thr Ile Asn Ser Arg 1360 1365 1370			576
TAC AAC GAC CTG ACC CGC CTG ATC GGC AAC TAC ACC GAC CAC GCC GTG Tyr Asn Asp Leu Thr Arg Leu Ile Gly Asn Tyr Thr Asp His Ala Val 1375 1380 1385			624
CGC TGG TAC AAC ACC GGC CTG GAG CGC GTG TGG GGT CCC GAC AGC CGC Arg Trp Tyr Asn Thr Gly Leu Glu Arg Val Trp Gly Pro Asp Ser Arg 1390 1395 1400 1405			672
GAC TGG ATC AGG TAC AAC CAG TTC CGC CGC GAG CTG ACC CTG ACC GTG Asp Trp Ile Arg Tyr Asn Gln Phe Arg Arg Glu Leu Thr Leu Thr Val 1410 1415 1420			720
CTG GAC ATC GTG AGC CTG TTC CCC AAC TAC GAC AGC CGC ACC TAC CCC Leu Asp Ile Val Ser Leu Phe Pro Asn Tyr Asp Ser Arg Thr Tyr Pro 1425 1430 1435			768
ATC CGC ACC GTG AGC CAG CTG ACC CGC GAG ATT TAC ACC AAC CCC GTG Ile Arg Thr Val Ser Gln Leu Thr Arg Glu Ile Tyr Thr Asn Pro Val 1440 1445 1450			816

CTG GAG AAC TTC GAC GGC AGC TTC CGC GGC AGC GCC CAG GGC ATC GAG Leu Glu Asn Phe Asp Gly Ser Phe Arg Gly Ser Ala Gln Gly Ile Glu 1455 1460 1465	864
GGC AGC ATC CGC AGC CCC CAC CTG ATG GAC ATC CTG AAC AGC ATC ACC Gly Ser Ile Arg Ser Pro His Leu Met Asp Ile Leu Asn Ser Ile Thr 1470 1475 1480 1485	912
ATC TAC ACC GAC GCC CAC CGC GGC GAG TAC TAC TGG AGC GGC CAC CAG Ile Tyr Thr Asp Ala His Arg Gly Glu Tyr Tyr Trp Ser Gly His Gln 1490 1495 1500	960
ATC ATG GCC AGC CCC GTC GGC TTC AGC GGC CCC GAG TTC ACC TTC CCC Ile Met Ala Ser Pro Val Gly Phe Ser Gly Pro Glu Phe Thr Phe Pro 1505 1510 1515	1008
CTG TAC GGC ACC ATG GGC AAC GCT GCA CCT CAG CAG CGC ATC GTG GCA Leu Tyr Gly Thr Met Gly Asn Ala Ala Pro Gln Gln Arg Ile Val Ala 1520 1525 1530	1056
CAG CTG GGC CAG GGA GTG TAC CGC ACC CTG AGC AGC ACC CTG TAC CGT Gln Leu Gly Gln Gly Val Tyr Arg Thr Leu Ser Ser Thr Leu Tyr Arg 1535 1540 1545	1104
CGA CCT TTC AAC ATC GGC ATC AAC AAC CAG CAG CTG AGC GTG CTG GAC Arg Pro Phe Asn Ile Gly Ile Asn Asn Gln Gln Leu Ser Val Leu Asp 1550 1555 1560 1565	1152
GGC ACC GAG TTC GCC TAC GGC ACC AGC AGC AAC CTG CCC AGC GCC GTG Gly Thr Glu Phe Ala Tyr Gly Thr Ser Ser Asn Leu Pro Ser Ala Val 1570 1575 1580	1200
TAC CGC AAG AGC GGC ACC GTG GAC AGC CTG GAC GAG ATC CCC CCT CAG Tyr Arg Lys Ser Gly Thr Val Asp Ser Leu Asp Glu Ile Pro Pro Gln 1585 1590 1595	1248
AAC AAC AAC GTG CCA CCT CGA CAG GGC TTC AGC CAC CGT CTG AGC CAC Asn Asn Asn Val Pro Pro Arg Gln Gly Phe Ser His Arg Leu Ser His 1600 1605 1610	1296
GTG AGC ATG TTC CGC AGT GGC TTC AGC AAC AGC AGC GTG AGC ATC ATC Val Ser Met Phe Arg Ser Gly Phe Ser Asn Ser Ser Val Ser Ile Ile 1615 1620 1625	1344
CGT GCA CCT ATG TTC AGC TGG ATT CAC CGC AGT GCC GAG TTC AAC AAC Arg Ala Pro Met Phe Ser Trp Ile His Arg Ser Ala Glu Phe Asn Asn 1630 1635 1640 1645	1392
ATC ATC CCC AGC AGC CAG ATC ACC CAG ATC CCC CTG ACC AAG AGC ACC Ile Ile Pro Ser Ser Gln Ile Thr Gln Ile Pro Leu Thr Lys Ser Thr 1650 1655 1660	1440
AAC CTG GGC AGC GGC ACC AGC GTG GTG AAG GGC CCC GGC TTC ACC GGC Asn Leu Gly Ser Gly Thr Ser Val Val Lys Gly Pro Gly Phe Thr Gly 1665 1670 1675	1488
GGC GAC ATC CTG CGC CGC ACC AGC CCC GGC CAG ATC AGC ACC CTG CGC Gly Asp Ile Leu Arg Arg Thr Ser Pro Gly Gln Ile Ser Thr Leu Arg 1680 1685 1690	1536

GTG	AAC	ATC	ACC	GCC	CCC	CTG	AGC	CAG	CGC	TAC	CGC	GTG	CGC	ATC	CGC	1582
Val	Asn	Ile	Thr	Ala	Pro	Leu	Ser	Gln	Arg	Tyr	Arg	Val	Arg	Ile	Arg	
1695						1700			1705							
TAC	GCC	AGC	ACC	ACC	AAC	CTG	CAG	TTC	CAC	ACC	AGC	ATC	GAC	GGC	CGC	1632
Tyr	Ala	Ser	Thr	Thr	Asn	Leu	Gln	Phe	His	Thr	Ser	Ile	Asp	Gly	Arg	
1710			1715						1720			1725				
CCC	ATC	AAC	CAG	GGC	AAC	TTC	AGC	GCC	ACC	ATG	AGC	AGC	GGC	AGC	AAC	1680
Pro	Ile	Asn	Gln	Gly	Asn	Phe	Ser	Ala	Thr	Met	Ser	Ser	Gly	Ser	Asn	
			1730			1735						1740				
CTG	CAG	AGC	GGC	AGC	TTC	CGC	ACC	GTG	GGC	TTC	ACC	ACC	CCC	TTC	AAC	1728
Leu	Gln	Ser	Gly	Ser	Phe	Arg	Thr	Val	Gly	Phe	Thr	Thr	Pro	Phe	Asn	
			1745			1750						1755				
TTC	AGC	AAC	GGC	AGC	AGC	GTG	TTC	ACC	CTG	AGC	GCC	CAC	GTG	TTC	AAC	1776
Phe	Ser	Asn	Gly	Ser	Ser	Val	Phe	Thr	Leu	Ser	Ala	His	Val	Phe	Asn	
1760						1765						1770				
AGC	GGC	AAC	GAG	GTG	TAC	ATC	GAC	CGC	ATC	GAG	TTC	GTG	CCC	GCC	GAG	1824
Ser	Gly	Asn	Glu	Val	Tyr	Ile	Asp	Arg	Ile	Glu	Phe	Val	Pro	Ala	Glu	
1775						1780						1785				
GTG	ACC	TTC	GAG	GCC	GAG	TAC	GAC	CTG	GAG	AGG	GCT	CAG	AAG	GCC	GTG	1872
Val	Thr	Phe	Glu	Ala	Glu	Tyr	Asp	Leu	Glu	Arg	Ala	Gln	Lys	Ala	Val	
1790			1795						1800						1805	
AAC	GAG	CTG	TTC	ACC	AGC	AGC	AAC	CAG	ATC	GGC	CTG	AAG	ACC	GAC	GTG	1920
Asn	Glu	Leu	Phe	Thr	Ser	Ser	Asn	Gln	Ile	Gly	Leu	Lys	Thr	Asp	Val	
			1810						1815						1820	
ACC	GAC	TAC	CAC	ATC	GAT	CAA	GTA	TCC	AAT	TTA	GTT	GAG	TGT	TTA	TCT	1968
Thr	Asp	Tyr	His	Ile	Asp	Gln	Val	Ser	Asn	Leu	Val	Glu	Cys	Leu	Ser	
			1825			1830						1835				
GAT	GAA	TTT	TGT	CTG	GAT	GAA	AAA	AAA	GAA	TTG	TCC	GAG	AAA	GTC	AAA	2016
Asp	Glu	Phe	Cys	Leu	Asp	Glu	Lys	Lys	Glu	Leu	Ser	Glu	Lys	Val	Lys	
1840						1845						1850				
CAT	GCG	AAG	CGA	CTT	AGT	GAT	GAG	CGG	AAT	TTA	CTT	CAA	GAT	CCA	AAC	2064
His	Ala	Lys	Arg	Leu	Ser	Asp	Glu	Arg	Asn	Leu	Leu	Gln	Asp	Pro	Asn	
1855						1860			1865							
TTT	AGA	GGG	ATC	AAT	AGA	CAA	CTA	GAC	CGT	GGC	TGG	AGA	GGA	AGT	ACG	2112
Phe	Arg	Gly	Ile	Asn	Arg	Gln	Leu	Asp	Arg	Gly	Trp	Arg	Gly	Ser	Thr	
1870			1875						1880						1885	
GAT	ATT	ACC	ATC	CAA	GGA	GGC	GAT	GAC	GTA	TTC	AAA	GAG	AAT	TAC	GTT	2160
Asp	Ile	Thr	Ile	Gln	Gly	Gly	Asp	Asp	Val	Phe	Lys	Glu	Asn	Tyr	Val	
			1890						1895						1900	
ACG	CTA	TTG	GGT	ACC	TTT	GAT	GAG	TGC	TAT	CCA	ACG	TAT	TTA	TAT	CAA	2208
Thr	Leu	Leu	Gly	Thr	Phe	Asp	Glu	Cys	Tyr	Pro	Thr	Tyr	Leu	Tyr	Gln	
			1905													

Gly	Tyr	Ile	Glu	Asp	Ser	Gln	Asp	Leu	Glu	Ile	Tyr	Leu	Ile	Arg	Tyr	
1935						1940				1945						
AAT	GCC	AAA	CAC	GAA	ACA	GTA	AAT	GTG	CCA	GGT	ACG	GGT	TCC	TTA	TGG	2352
Asn	Ala	Lys	His	Glu	Thr	Val	Asn	Val	Pro	Gly	Thr	Gly	Ser	Leu	Trp	
1950					1955				1960					1965		
CCG	CTT	TCA	GCC	CCA	AGT	CCA	ATC	GGC	AAG	TGC	GGG	GAG	CCG	AAT	CGA	2400
Pro	Leu	Ser	Ala	Pro	Ser	Pro	Ile	Gly	Lys	Cys	Gly	Glu	Pro	Asn	Arg	
				1970				1975					1980			
TGC	GCT	CCG	CAC	CTG	GAG	TGG	AAC	CCG	GAC	CTA	GAC	TGC	AGC	TGC	AGG	2448
Cys	Ala	Pro	His	Leu	Glu	Trp	Asn	Pro	Asp	Leu	Asp	Cys	Ser	Cys	Arg	
			1985				1990					1995				
GAC	GGG	GAG	AAG	TGC	GCC	CAC	CAC	AGC	CAC	CAC	TTC	AGC	CTG	GAC	ATC	2496
Asp	Gly	Glu	Lys	Cys	Ala	His	His	Ser	His	His	Phe	Ser	Leu	Asp	Ile	
			2000				2005					2010				
GAC	GTG	GGC	TGC	ACC	GAC	CTG	AAC	GAG	GAC	CTG	GGC	GTG	TGG	GTG	ATC	2544
Asp	Val	Gly	Cys	Thr	Asp	Leu	Asn	Glu	Asp	Leu	Gly	Val	Trp	Val	Ile	
						2020				2025						
TTC	AAG	ATC	AAG	ACC	CAG	GAC	GGC	CAC	GCC	CGC	CTG	GGC	AAT	CTA	GAA	2592
Phe	Lys	Ile	Lys	Thr	Gln	Asp	Gly	His	Ala	Arg	Leu	Gly	Asn	Leu	Glu	
2030					2035				2040					2045		
TTT	CTC	GAA	GAG	AAA	CCA	TTA	GTA	GGA	GAA	GCA	CTA	GCT	CGT	GTG	AAA	2640
Phe	Leu	Glu	Glu	Lys	Pro	Leu	Val	Gly	Glu	Ala	Leu	Ala	Arg	Val	Lys	
			2050				2055					2060				
AGA	GCG	GAG	AAA	AAA	TGG	AGA	GAC	AAA	CGT	GAA	AAA	TTG	GAA	TGG	GAA	2688
Arg	Ala	Glu	Lys	Lys	Trp	Arg	Asp	Lys	Arg	Glu	Lys	Leu	Glu	Trp	Glu	
			2065				2070					2075				
ACA	AAT	ATT	GTT	TAT	AAA	GAG	GCA	AAA	GAA	TCT	GTA	GAT	GCT	TTA	TTT	2736
Thr	Asn	Ile	Val	Tyr	Lys	Glu	Ala	Lys	Glu	Ser	Val	Asp	Ala	Leu	Phe	
			2080				2085					2090				
GTA	AAC	TCT	CAA	TAT	GAT	AGA	TTA	CAA	GCG	GAT	ACC	AAC	ATC	GCG	ATG	2784
Val	Asn	Ser	Gln	Tyr	Asp	Arg	Leu	Gln	Ala	Asp	Thr	Asn	Ile	Ala	Met	
			2095				2100				2105					
ATT	CAT	GCG	GCA	GAT	AAA	CGC	GTT	CAT	AGC	ATT	CGA	GAA	GCT	TAT	CTG	2832
Ile	His	Ala	Ala	Asp	Lys	Arg	Val	His	Ser	Ile	Arg	Glu	Ala	Tyr	Leu	
2110					2115				2120					2125		
CCT	GAG	CTG	TCT	GTG	ATT	CCG	GGT	GTC	AAT	GCG	GCT	ATT	TTT	GAA	GAA	2880
Pro	Glu	Leu	Ser	Val	Ile	Pro	Gly	Val	Asn	Ala	Ala	Ile	Phe	Glu	Glu	
			2130				2135					2140				
TTA	GAA	GGG	CGT	ATT	TTC	ACT	GCA	TTC	TCC	CTA	TAT	GAT	GCG	AGA	AAT	2928
Leu	Glu	Gly	Arg	Ile	Phe	Thr	Ala	Phe	Ser	Leu	Tyr	Asp	Ala	Arg	Asn	
			2145				2150					2155				
GTC	ATT	AAA	AAT	GGT	GAT	TTT	AAT	AAT	GGC	TTA	TCC	TGC	TGG	AAC	GTG	2976
Val	Ile	Lys	Asn	Gly	Asp	Phe	Asn	Asn	Gly	Leu	Ser	Cys	Trp	Asn	Val	
			2160				2165					2170				
AAA	GGG	CAT	GTA	GAT	GTA	GAA	GAA	CAA	AAC	AAC	CAC	CGT	TCG	GTC	CTT	3024
Lys	Gly	His	Val	Asp	Val	Glu	Glu	Gln	Asn	Asn	His	Arg	Ser	Val	Leu	

2175	2180	2185	
GTT GTT CCG GAA TGG	GAA GCA GAA GTG	TCA CAA GAA GTT CGT GTC TGT	3072
Val Val Pro Glu Trp	Glu Ala Glu Val Ser	Gln Glu Val Arg Val Cys	
2190	2195	2200 2205	
CCG GGT CGT GGC TAT ATC CTT CGT GTC	ACA GCG TAC AAG GAG GGA TAT		3120
Pro Gly Arg Gly Tyr Ile Leu Arg Val	Thr Ala Tyr Lys Glu Gly Tyr		
	2210 2215	2220	
GGA GAA GGT TGC GTA ACC ATT CAT GAG ATC GAG AAC AAT ACA GAC GAA			3168
Gly Glu Gly Cys Val Thr Ile His Glu Ile Glu Asn Asn Thr Asp Glu			
	2225 2230	2235	
CTG AAG TTT AGC AAC TGT GTA GAA GAG GAA GTA TAT CCA AAC AAC ACG			3216
Leu Lys Phe Ser Asn Cys Val Glu Glu Glu Val Tyr Pro Asn Asn Thr			
	2240 2245	2250	
GTA ACG TGT AAT GAT TAT ACT GCG ACT CAA GAA GAA TAT GAG GGT ACG			3264
Val Thr Cys Asn Asp Tyr Thr Ala Thr Gln Glu Glu Tyr Glu Gly Thr			
	2255 2260	2265	
TAC ACT TCT CGT AAT CGA GGA TAT GAC GGA GCC TAT GAA AGC AAT TCT			3312
Tyr Thr Ser Arg Asn Arg Gly Tyr Asp Gly Ala Tyr Glu Ser Asn Ser			
	2270 2275	2280 2285	
TCT GTA CCA GCT GAT TAT GCA TCA GCC TAT GAA GAA AAA GCA TAT ACA			3360
Ser Val Pro Ala Asp Tyr Ala Ser Ala Tyr Glu Glu Lys Ala Tyr Thr			
	2290 2295	2300	
GAT GGA CGA AGA GAC AAT CCT TGT GAA TCT AAC AGA GGA TAT GGG GAT			3408
Asp Gly Arg Arg Asp Asn Pro Cys Glu Ser Asn Arg Gly Tyr Gly Asp			
	2305 2310	2315	
TAC ACA CCA CTA CCA GCT GGC TAT GTG ACA AAA GAA TTA GAG TAC TTC			3456
Tyr Thr Pro Leu Pro Ala Gly Tyr Val Thr Lys Glu Leu Glu Tyr Phe			
	2320 2325	2330	
CCA GAA ACC GAT AAG GTA TGG ATT GAG ATC GGA GAA ACG GAA GGA ACA			3504
Pro Glu Thr Asp Lys Val Trp Ile Glu Ile Gly Glu Thr Glu Gly Thr			
	2335 2340	2345	
TTC ATC GTG GAC AGC GTG GAA TTA CTT CTT ATG GAG GAA TAAG			3547
Phe Ile Val Asp Ser Val Glu Leu Leu Leu Met Glu Glu			
	2350 2355	2360	

(2) INFORMATION FOR SEQ ID NO:17:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1181 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

Met	Asp	Asn	Asn	Pro	Asn	Ile	Asn	Glu	Cys	Ile	Pro	Tyr	Asn	Cys	Leu
1				5				10						15	

Ser Asn Pro Glu Val Glu Val Leu Gly Gly Glu Arg Ile Glu Thr Gly
20 25 30

Tyr Thr Pro Ile Asp Ile Ser Leu Ser Leu Thr Gln Phe Leu Leu Ser
35 40 45

Glu Phe Val Pro Gly Ala Gly Phe Val Leu Gly Leu Val Asp Ile Ile
50 55 60

Trp Gly Ile Phe Gly Pro Ser Gln Trp Asp Ala Phe Leu Val Gln Ile
65 70 75 80

Glu Gln Leu Ile Asn Gln Arg Ile Glu Glu Phe Ala Arg Asn Gln Ala
85 90 95

Ile Ser Arg Leu Glu Gly Leu Ser Asn Leu Tyr Gln Ile Tyr Ala Glu
100 105 110

Ser Phe Arg Glu Trp Glu Ala Asp Pro Thr Asn Pro Ala Leu Arg Glu
115 120 125

Glu Met Arg Ile Gln Phe Asn Asp Met Asn Ser Ala Leu Thr Thr Ala
130 135 140

Ile Pro Leu Phe Ala Val Gln Asn Tyr Gln Val Pro Leu Leu Ser Val
145 150 155 160

Tyr Val Gln Ala Ala Asn Leu His Leu Ser Val Leu Arg Asp Val Ser
165 170 175

Val Phe Gly Gln Arg Trp Gly Phe Asp Ala Ala Thr Ile Asn Ser Arg
180 185 190

Tyr Asn Asp Leu Thr Arg Leu Ile Gly Asn Tyr Thr Asp His Ala Val
195 200 205

Arg Trp Tyr Asn Thr Gly Leu Glu Arg Val Trp Gly Pro Asp Ser Arg
210 215 220

Asp Trp Ile Arg Tyr Asn Gln Phe Arg Arg Glu Leu Thr Leu Thr Val
225 230 235 240

Leu Asp Ile Val Ser Leu Phe Pro Asn Tyr Asp Ser Arg Thr Tyr Pro
245 250 255

Ile Arg Thr Val Ser Gln Leu Thr Arg Glu Ile Tyr Thr Asn Pro Val
260 265 270

Leu Glu Asn Phe Asp Gly Ser Phe Arg Gly Ser Ala Gln Gly Ile Glu
275 280 285

Gly Ser Ile Arg Ser Pro His Leu Met Asp Ile Leu Asn Ser Ile Thr
290 295 300

Ile Tyr Thr Asp Ala His Arg Gly Glu Tyr Tyr Trp Ser Gly His Gln
305 310 315 320

Ile Met Ala Ser Pro Val Gly Phe Ser Gly Pro Glu Phe Thr Phe Pro
325 330 335

Leu Tyr Gly Thr Met Gly Asn Ala Ala Pro Gln Gln Arg Ile Val Ala

340				345				350							
Gln	Leu	Gly 355	Gln	Gly	Val	Tyr	Arg 360	Thr	Leu	Ser	Ser	Thr 365	Leu	Tyr	Arg
Arg	Pro 370	Phe	Asn	Ile	Gly	Ile 375	Asn	Asn	Gln	Gln	Leu 380	Ser	Val	Leu	Asp
Gly 385	Thr	Glu	Phe	Ala	Tyr 390	Gly	Thr	Ser	Ser	Asn 395	Leu	Pro	Ser	Ala	Val 400
Tyr	Arg	Lys	Ser	Gly 405	Thr	Val	Asp	Ser	Leu 410	Asp	Glu	Ile	Pro	Pro 415	Gln
Asn	Asn	Asn	Val 420	Pro	Pro	Arg	Gln	Gly 425	Phe	Ser	His	Arg	Leu 430	Ser	His
Val	Ser	Met 435	Phe	Arg	Ser	Gly	Phe 440	Ser	Asn	Ser	Ser	Val 445	Ser	Ile	Ile
Arg	Ala 450	Pro	Met	Phe	Ser	Trp 455	Ile	His	Arg	Ser	Ala 460	Glu	Phe	Asn	Asn
Ile 465	Ile	Pro	Ser	Ser	Gln 470	Ile	Thr	Gln	Ile	Pro 475	Leu	Thr	Lys	Ser	Thr 480
Asn	Leu	Gly	Ser	Gly 485	Thr	Ser	Val	Val	Lys 490	Gly	Pro	Gly	Phe	Thr 495	Gly
Gly	Asp	Ile 500	Leu	Arg	Arg	Thr	Ser	Pro 505	Gly	Gln	Ile	Ser	Thr 510	Leu	Arg
Val	Asn	Ile 515	Thr	Ala	Pro	Leu	Ser 520	Gln	Arg	Tyr	Arg	Val 525	Arg	Ile	Arg
Tyr	Ala 530	Ser	Thr	Thr	Asn 535	Leu	Gln	Phe	His	Thr	Ser 540	Ile	Asp	Gly	Arg
Pro 545	Ile	Asn	Gln	Gly	Asn 550	Phe	Ser	Ala	Thr	Met 555	Ser	Ser	Gly	Ser	Asn 560
Leu	Gln	Ser	Gly	Ser 565	Phe	Arg	Thr	Val	Gly 570	Phe	Thr	Thr	Pro	Phe 575	Asn
Phe	Ser	Asn 580	Gly	Ser	Ser	Val	Phe 585	Thr	Leu	Ser	Ala	His 590	Val	Phe	Asn
Ser	Gly	Asn 595	Glu	Val	Tyr	Ile	Asp 600	Arg	Ile	Glu	Phe	Val 605	Pro	Ala	Glu
Val	Thr 610	Phe	Glu	Ala	Glu 615	Tyr	Asp	Leu	Glu	Arg	Ala 620	Gln	Lys	Ala	Val
Asn 625	Glu	Leu	Phe	Thr 630	Ser	Ser	Asn	Gln	Ile	Gly 635	Leu	Lys	Thr	Asp	Val 640
Thr	Asp	Tyr	His 645	Ile	Asp	Gln	Val	Ser	Asn 650	Leu	Val	Glu	Cys	Leu 655	Ser
Asp	Glu	Phe 660	Cys	Leu	Asp	Glu	Lys 665	Lys	Glu	Leu	Ser	Glu	Lys 670	Val	Lys

Lys Gly His Val Asp Val Glu Glu Gln Asn Asn His Arg Ser Val Leu
 995 1000 1005
 Val Val Pro Glu Trp Glu Ala Glu Val Ser Gln Glu Val Arg Val Cys
 1010 1015 1020
 Pro Gly Arg Gly Tyr Ile Leu Arg Val Thr Ala Tyr Lys Glu Gly Tyr
 1025 1030 1035 1040
 Gly Glu Gly Cys Val Thr Ile His Glu Ile Glu Asn Asn Thr Asp Glu
 1045 1050 1055
 Leu Lys Phe Ser Asn Cys Val Glu Glu Glu Val Tyr Pro Asn Asn Thr
 1060 1065 1070
 Val Thr Cys Asn Asp Tyr Thr Ala Thr Gln Glu Glu Tyr Glu Gly Thr
 1075 1080 1085
 Tyr Thr Ser Arg Asn Arg Gly Tyr Asp Gly Ala Tyr Glu Ser Asn Ser
 1090 1095 1100
 Ser Val Pro Ala Asp Tyr Ala Ser Ala Tyr Glu Glu Lys Ala Tyr Thr
 1105 1110 1115 1120
 Asp Gly Arg Arg Asp Asn Pro Cys Glu Ser Asn Arg Gly Tyr Gly Asp
 1125 1130 1135
 Tyr Thr Pro Leu Pro Ala Gly Tyr Val Thr Lys Glu Leu Glu Tyr Phe
 1140 1145 1150
 Pro Glu Thr Asp Lys Val Trp Ile Glu Ile Gly Glu Thr Glu Gly Thr
 1155 1160 1165
 Phe Ile Val Asp Ser Val Glu Leu Leu Leu Met Glu Glu
 1170 1175 1180

(2) INFORMATION FOR SEQ ID NO:18:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 4817 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: join(1839..2141, 2239..2547, 2641..2718, 2794..2871, 3001..3135, 3236..3370)
- (D) OTHER INFORMATION: /product= "maize TrpA"

/note= "Maize TrpA sequence as disclosed in Figure 24."

(ix) FEATURE:

- (A) NAME/KEY: TATA_signal
- (B) LOCATION: 1594..1599

(ix) FEATURE:

(A) NAME/KEY: CAAT_signal
(B) LOCATION: 1495..1499

(ix) FEATURE:

(A) NAME/KEY: promoter
(B) LOCATION: 39..1838
(D) OTHER INFORMATION: /function= "Promoter sequence used
in pCIB4433"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

GAATTCGGAT CCATTAAAGA AGTCTTTGAA CAGATTCTAG AGATCTAGTT TAATGAGCTC	60
CCAAAAGTCT TGAAAAAATT CAGCGGGGAG GCCATTAGGG CAGGGGTACT GTTATGTTTT	120
AAAGAGAACA CCACTTTCTT GATCTCTTCT AAAGAGAAAT GTTTTGTAAG AAGGATCCTG	180
TCCTCCTCAT CCAACCTTTT CATCGGCAAA TTTTTCATAG AGATATTAGA GGCAAGAGAG	240
GGGCCAAAAA GATCCATGTA AATGGAAGTG GCCACCTGGT TGATACCTCC CTCATCTTCA	300
ACAGAAAATC CATTATGAAA AAGTGAATGG ATTTTAAACT CTTCTTTTTC TTCCCTTTTG	360
CAATGAGCTG AAAATATCTG GTATTATTCT CATCACCTC ATTAATGAAT CTGTCCCTAG	420
CAATTTGCTT TCTCTTGATC CCTTCTGCAG CCACCATGTT TCTTAAATTC CACTCCATAT	480
CAAGCTTTTC CAATCTATCA GAATCTGAGA TGGCTGCAAT CTCTCTCATT TTCTCAAGGA	540
TATCGATGTT ATCCATAAGG TATTTCTTGA ACTTCTTATA TTTCCCTTCG ACATTTATAT	600
TCCATCCTTT CAACATTTTT TTGTTCAATC TTTTTTGTTT TTTTCCTTTC CAAACATCGA	660
TACATTTTCT GCTCCTCACA GGTAAGGACG AGCTTTCAAA AAACCTTCTG CTTTAAAGTC	720
AGGTCTGAGC CTCCAGCAAA GCTCACATAT CTAAAGTCCC TCTTCTTAGT TGGGACAGAG	780
TCAGTGCTAA GACACATGGG AACATGACCA GAAAAAAAAA ATCATATTTA GCCCAGAGAC	840
AACAATATTC TTGTACTGCA AGTCTCGTTA TGGGCTAGCA AAGGAATCTA CCCAACTTCT	900
CAAATGTGTT GGGATGTCAA GTATATAGAC TATTCATCAG TTCCAACCTCT ATCAAACCTGT	960
GCAGCTCAAT TATAGAGTTG AATAAAGTGC TCCATCTATT TGTTCTTATC CTCATATTTG	1020
GTAAAGATAT TAAAATCACC TCCCACCAAC ATTTAAAGTG CACCATTTAA AGTGGCTCGC	1080
GAGCACCAAA CCGCTGAAAA CCGGAAATGT TTAGCACGTT GGCAGCGGGA CCCTTTTCTA	1140
TCTCATCGTG TTCTTCGTTG TCCACCACGG CCCACGGGCC AACGCTCCTC CATCCTGTAG	1200
TGTAGAGTAT ATTCCATTTG CGACCGAGCC GAGCATCGAT CCAGCCACAC TGGCCACTGC	1260
CAGCCAGCCA TGTGGCACTC CTACGTATAC TACGTGAGGT GAGATTCACT CACATGGGAT	1320
GGGACCGAGA TATTTTACTG CTGTGGTTGT GTGAGAGATA ATAAAGCATT TATGACGATT	1380
GCTGAACAGC ACACACCATG CGTCCAGATA GAGAAAGCTT TCTCTCTTTA TTCGCATGCA	1440
TGTTTCATTA TCTTTTATCA TATATATATA ACACATATTA AATGATTCTT CGTTCCAATT	1500

TATAATTCAT TTGACTTTTT TATCCACCGA TGCTCGTTTT ATTAAAAAAA ATATTATAAT	1560
TATTGTTACT TTTTGTGTA ATATTGTTTA GCATATAATA AACTTTGATA CTAGTATGTT	1620
TCCGAGCAAA AAAAAATATT AATATTTAGA TTACGAGCCC ATTAATTAAT TATATTCGAG	1680
ACAAGCGAAG CAAAGCAAAG CAAGCTAATG TTGCCCTGCG TGTGCATGCA GAGGCCCCGCT	1740
CTTGCTATAA ACGAGGCAGC TAGACGCGAC TCGACTCATC AGCCTCATCA ACCTCGACGA	1800
AGGAGGAACG AACGGACAGG TTGTTGCACA GAAGCGAC ATG GCT TTC GCG CCC	1853
Met Ala Phe Ala Pro	
1 5	
AAA ACG TCC TCC TCC TCC TCG CTG TCC TCG GCG TTG CAG GCA GCT CAG	1901
Lys Thr Ser Ser Ser Ser Ser Leu Ser Ser Ala Leu Gln Ala Ala Gln	
10 15 20	
TCG CCG CCG CTG CTC CTG AGG CGG ATG TCG TCG ACC GCA ACA CCG AGA	1949
Ser Pro Pro Leu Leu Leu Arg Arg Met Ser Ser Thr Ala Thr Pro Arg	
25 30 35	
CGG AGG TAC GAC GCG GCC GTC GTC GTC ACT ACC ACC ACC ACT GCT AGA	1997
Arg Arg Tyr Asp Ala Ala Val Val Val Thr Thr Thr Thr Thr Ala Arg	
40 45 50	
GCT GCG GCG GCT GCT GTC ACG GTT CCC GCC GCC CCG CCG CAG GCG GGC	2045
Ala Ala Ala Ala Ala Val Thr Val Pro Ala Ala Pro Pro Gln Ala Gly	
55 60 65	
CGC CGC CGC CGG TGC CAC CAA AGC AAG CGG CGG CAC CCG CAG AGG AGG	2093
Arg Arg Arg Arg Cys His Gln Ser Lys Arg Arg His Pro Gln Arg Arg	
70 75 80 85	
AGC CGT CCG GTG TCG GAC ACC ATG GCG GCG CTC ATG GCC AAG GGC AAG	2141
Ser Arg Pro Val Ser Asp Thr Met Ala Ala Leu Met Ala Lys Gly Lys	
90 95 100	
GTTCGTATAG TACGCGCGCG TGTCGTCGTC GTTATTTTGC GCATAGGCGC GGACATACAC	2201
GTGCTTTAGC TAGCTAACAG CTAGATCATC GGTGCAG ACG GCG TTC ATC CCG TAC	2256
Thr Ala Phe Ile Pro Tyr	
105	
ATC ACC GCC GGC GAC CCG GAC CTA GCG ACG ACG GCC GAG GCG CTG CGT	2304
Ile Thr Ala Gly Asp Pro Asp Leu Ala Thr Thr Ala Glu Ala Leu Arg	
110 115 120	
CTG CTG GAC GGC TGT GGC GCC GAC GTC ATC GAG CTG GGG GTA CCC TGC	2352
Leu Leu Asp Gly Cys Gly Ala Asp Val Ile Glu Leu Gly Val Pro Cys	
125 130 135	
TCG GAC CCC TAC ATC GAC GGG CCC ATC ATC CAG GCG TCG GTG GCG CGG	2400
Ser Asp Pro Tyr Ile Asp Gly Pro Ile Ile Gln Ala Ser Val Ala Arg	
140 145 150 155	
GCT CTG GCC AGC GGC ACC ACC ATG GAC GCC GTG CTG GAG ATG CTG AGG	2448
Ala Leu Ala Ser Gly Thr Thr Met Asp Ala Val Leu Glu Met Leu Arg	
160 165 170	

GAG GTG ACG CCG GAG CTG TCG TGC CCC GTG GTG CTC CTC TCC TAC TAC Glu Val Thr Pro Glu Leu Ser Cys Pro Val Val Leu Leu Ser Tyr Tyr 175 180 185	2496
AAG CCC ATC ATG TCT CGC AGC TTG GCC GAG ATG AAA GAG GCG GGG GTC Lys Pro Ile Met Ser Arg Ser Leu Ala Glu Met Lys Glu Ala Gly Val 190 195 200	2544
CAC GGTAAC TATA GCTAGCTCTT CCGATCCCCC TTCAATTAAT TAATTTATAG His	2597
TAGTCCATTC ATGTGATGAT TTTTGTTTTT CTTTTTACTG ACA GGT CTT ATA GTG Gly Leu Ile Val 205	2652
CCT GAT CTC CCG TAC GTG GCC GCG CAC TCG CTG TGG AGT GAA GCC AAG Pro Asp Leu Pro Tyr Val Ala Ala His Ser Leu Trp Ser Glu Ala Lys 210 215 220	2700
AAC AAC AAC CTG GAG CTG GTAGGTTGAA TTAAGTTGAT GCATGTGATG Asn Asn Asn Leu Glu Leu 225 230	2748
ATTTATGTAG CTAGATCGAG CTAGCTATAA TTAGGAGCAT ATCAG GTG CTG CTG Val Leu Leu	2802
ACA ACA CCA GCC ATA CCA GAA GAC AGG ATG AAG GAG ATC ACC AAG GCT Thr Thr Pro Ala Ile Pro Glu Asp Arg Met Lys Glu Ile Thr Lys Ala 235 240 245	2850
TCA GAA GGC TTC GTC TAC CTG GTAGTTATAT GTATATATAG ATGGACGACG Ser Glu Gly Phe Val Tyr Leu 250 255	2901
TAACTCATTC CAGCCCCATG CATATATGGA GGCTTCAATT CTGCAGAGAC GACGAAGACC	2961
ACGACGACGA CTAACACTAG CTAGGGGCGT ACGTTGCAG GTG AGC GTG AAC GGA Val Ser Val Asn Gly 260	3015
GTG ACA GGT CCT CGC GCA AAC GTG AAC CCA CGA GTG GAG TCA CTC ATC Val Thr Gly Pro Arg Ala Asn Val Asn Pro Arg Val Glu Ser Leu Ile 265 270 275	3063
CAG GAG GTT AAG AAG GTG ACT AAC AAG CCC GTT GCT GTT GGC TTC GGC Gln Glu Val Lys Lys Val Thr Asn Lys Pro Val Ala Val Gly Phe Gly 280 285 290	3111
ATA TCC AAG CCC GAG CAC GTG AAG CAGGTACGTA CGTAGCTGAC CAAAAAAAC Ile Ser Lys Pro Glu His Val Lys 295 300	3165
TGTTAACAAG TTTTGTTTGA CAAGCCGGCT ACTAGCTAGC TAACAGTGAT CAGTGACACA	3225
CACACACACA CAG ATT GCG CAG TGG GGC GCT GAC GGG GTG ATC ATC GGC Gln Ile Ala Gln Trp Gly Ala Asp Gly Val Ile Ile Gly 305 310	3274
AGC GCC ATG GTG AGG CAG CTG GGC GAA GCG GCT TCT CCC AAG CAA GGC	3322

Ser	Ala	Met	Val	Arg	Gln	Leu	Gly	Glu	Ala	Ala	Ser	Pro	Lys	Gln	Gly	
315					320					325					330	
CTG	AGG	AGG	CTG	GAG	GAG	TAT	GCC	AGG	GGC	ATG	AAG	AAC	GCG	CTG	CCA	3370
Leu	Arg	Arg	Leu	Glu	Glu	Tyr	Ala	Arg	Gly	Met	Lys	Asn	Ala	Leu	Pro	
			335						340					345		
TGAGTCCATG	ACAAAGTAAA	ACGTACAGAG	ACACTTGATA	ATATCTATCT	ATCATCTCGG											3430
AGAAGACGAC	CGACCAATAA	AAATAAGCCA	AGTGAAGTG	AAGCTTAGCT	GTATATACAC											3490
CGTACGTCGT	CGTCGTCGTT	CCGGATCGAT	CTCGGCCGGC	TAGCTAGCAG	AACGTGTACG											3550
TAGTAGTATG	TAATGCATGG	AGTGTGGAGC	TACTAGCTAG	CTGGCCGTTT	ATTTCGATTAT											3610
AATTCTTCGC	TCTGCTGTGG	TAGCAGATGT	ACCTAGTCGA	TCTTGTACGA	CGAAGAAGCT											3670
GGCTAGCTAG	CCGTCTCGAT	CGTATATGTA	CTGATTAATC	TGCAGATTGA	ATAAAAACTA											3730
CAGTACGCAT	ATGATGCGTA	CGTACGTGTG	TATAGTTTGT	GCTCATATAT	GCTCCTCATC											3790
ACCTGCCTGA	TCTGCCCATC	GATCTCTCTC	GTACTCCTTC	CTGTTAAATG	CCTTCTTTGA											3850
CAGACACACC	ACCACCAGCA	GCAGTGACGC	TCTGCACGCC	GCCGCTTTAA	GACATGTAAG											3910
ATATTTTAAG	AGGTATAAGA	TACCAAGGAG	CACAAATCTG	GAGCACTGGG	ATATTGCAAA											3970
GACAAAAAAA	AAACAAAATT	AAAGTCCCAC	CAAAGTAGAG	ATAGTAAAGA	GGTGGATGGA											4030
TTAAATTTAT	CTCATGATTT	TTGGATCTGC	TCAAATAGAT	CGATATGGTA	TTCAGATCTA											4090
TGTTGTATAG	CCTTTTCATT	AGCTTTCTGA	AAAAAAATG	GTATGATGAG	TGCGGAGTAG											4150
CTAGGGCTGT	GAAGGAGTCG	GATGGGCTTC	CACGTACTTG	TTTGTGGCCC	TAGTCCGGTT											4210
CTATTTAGGT	CCGATCCGAG	TCCGGCATGG	TCCGGTTCCA	TACGGGCTAG	GACCAAGCTC											4270
GGCACGTGAG	TTTTAGGCCC	GTCGGCTAGC	CCGAGCACGA	CCCCTTTTTA	AACTGGCTAG											4330
GACTCGCCCA	TTTAATAAGA	CAAACATTGC	AAAAAATAGC	TCTATTTTTT	ATTTAAAATA											4390
TATTGTTTAT	TTGTGAAATG	TGTATTATTT	GTAATATATA	TTATTGTATA	TAGTTATATC											4450
TTCAATTATG	ATTTATAAAT	ATGTTTTTTA	TTATGAACTC	AATTTTAAGT	TTGATTTATG											4510
CGTTGGCGGG	CTCGAGGAGG	CACGGTGAAC	ATTTTTGGGT	CGGGCTTAAC	GGGTCGGCCC											4570
GGCCCGGTTT	GGCCCATCCA	CGGCCCATCC	CGTGTCGGCC	TCGTTCGGTG	AGTTCAGCCC											4630
GTCGGACAAC	CCGTCCCCGG	CCCGGATAAT	TAATCGGGCC	TAACCGTGGC	GTGCTTAAAC											4690
GGTCCGTGCC	TCAACGGACC	GGGCCGCGGG	CGGCCCGTTT	GACATCTCTA	GTGGTGTGAT											4750
TAGAGATGGC	GATGGGAACC	GATCACTGAT	TCCGTGTGGA	GAATTCGATA	TCAAGCTTAT											4810
CGATACC																4817

(2) INFORMATION FOR SEQ ID NO:19:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 346 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:

```

Met Ala Phe Ala Pro Lys Thr Ser Ser Ser Ser Ser Leu Ser Ser Ala
 1           5           10           15
Leu Gln Ala Ala Gln Ser Pro Pro Leu Leu Leu Arg Arg Met Ser Ser
          20           25           30
Thr Ala Thr Pro Arg Arg Arg Tyr Asp Ala Ala Val Val Val Thr Thr
 35           40           45
Thr Thr Thr Ala Arg Ala Ala Ala Ala Val Thr Val Pro Ala Ala
 50           55           60
Pro Pro Gln Ala Gly Arg Arg Arg Arg Cys His Gln Ser Lys Arg Arg
 65           70           75           80
His Pro Gln Arg Arg Ser Arg Pro Val Ser Asp Thr Met Ala Ala Leu
          85           90           95
Met Ala Lys Gly Lys Thr Ala Phe Ile Pro Tyr Ile Thr Ala Gly Asp
          100          105          110
Pro Asp Leu Ala Thr Thr Ala Glu Ala Leu Arg Leu Leu Asp Gly Cys
          115          120          125
Gly Ala Asp Val Ile Glu Leu Gly Val Pro Cys Ser Asp Pro Tyr Ile
          130          135          140
Asp Gly Pro Ile Ile Gln Ala Ser Val Ala Arg Ala Leu Ala Ser Gly
          145          150          155          160
Thr Thr Met Asp Ala Val Leu Glu Met Leu Arg Glu Val Thr Pro Glu
          165          170          175
Leu Ser Cys Pro Val Val Leu Leu Ser Tyr Tyr Lys Pro Ile Met Ser
          180          185          190
Arg Ser Leu Ala Glu Met Lys Glu Ala Gly Val His Gly Leu Ile Val
          195          200          205
Pro Asp Leu Pro Tyr Val Ala Ala His Ser Leu Trp Ser Glu Ala Lys
          210          215          220
Asn Asn Asn Leu Glu Leu Val Leu Leu Thr Thr Pro Ala Ile Pro Glu
          225          230          235          240
Asp Arg Met Lys Glu Ile Thr Lys Ala Ser Glu Gly Phe Val Tyr Leu
          245          250          255
Val Ser Val Asn Gly Val Thr Gly Pro Arg Ala Asn Val Asn Pro Arg
          260          265          270
Val Glu Ser Leu Ile Gln Glu Val Lys Lys Val Thr Asn Lys Pro Val
          275          280          285

```

Ala Val Gly Phe Gly Ile Ser Lys Pro Glu His Val Lys Gln Ile Ala
 290 295 300

Gln Trp Gly Ala Asp Gly Val Ile Ile Gly Ser Ala Met Val Arg Gln
 305 310 315 320

Leu Gly Glu Ala Ala Ser Pro Lys Gln Gly Leu Arg Arg Leu Glu Glu
 325 330 335

Tyr Ala Arg Gly Met Lys Asn Ala Leu Pro
 340 345

(2) INFORMATION FOR SEQ ID NO:20:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1349 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 3..1226
- (D) OTHER INFORMATION: /note= "cDNA sequence for maize pollen-specific calcium dependent protein kinase gene as disclosed in Figure 30."

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:20:

TG CAG ATC ATG CAC CAC CTC TCC GGC CAG CCC AAC GTG GTG GGC CTC Gln Ile Met His His Leu Ser Gly Gln Pro Asn Val Val Gly Leu 350 355 360	47
CGC GGC GCG TAC GAG GAC AAG CAG AGC GTG CAC CTC GTC ATG GAG CTG Arg Gly Ala Tyr Glu Asp Lys Gln Ser Val His Leu Val Met Glu Leu 365 370 375	95
TGC GCG GGC GGG GAG CTC TTC GAC CGC ATC ATC GCC CGG GGC CAG TAC Cys Ala Gly Gly Glu Leu Phe Asp Arg Ile Ile Ala Arg Gly Gln Tyr 380 385 390	143
ACG GAG CGC GGC GCC GCG GAG CTG CTG CGC GCC ATC GTG CAG ATC GTG Thr Glu Arg Gly Ala Ala Glu Leu Leu Arg Ala Ile Val Gln Ile Val 395 400 405	191
CAC ACC TGC CAC TCC ATG GGG GTG ATG CAC CGG GAC ATC AAG CCC GAG His Thr Cys His Ser Met Gly Val Met His Arg Asp Ile Lys Pro Glu 410 415 420 425	239
AAC TTC CTG CTG CTC AGC AAG GAC GAG GAC GCG CCG CTC AAG GCC ACC Asn Phe Leu Leu Leu Ser Lys Asp Glu Asp Ala Pro Leu Lys Ala Thr 430 435 440	287
GAC TTC GGC CTC TCC GTC TTC TTC AAG GAG GGC GAG CTG CTC AGG GAC	335

Asp	Phe	Gly	Leu	Ser	Val	Phe	Phe	Lys	Glu	Gly	Glu	Leu	Leu	Arg	Asp	
			445					450					455			
ATC	GTC	GGC	AGC	GCC	TAC	TAC	ATC	GCG	CCC	GAG	GTG	CTC	AAG	AGG	AAG	383
Ile	Val	Gly	Ser	Ala	Tyr	Tyr	Ile	Ala	Pro	Glu	Val	Leu	Lys	Arg	Lys	
		460					465					470				
TAC	GGC	CCG	GAG	GCC	GAC	ATC	TGG	AGC	GTC	GGC	GTC	ATG	CTC	TAC	ATC	431
Tyr	Gly	Pro	Glu	Ala	Asp	Ile	Trp	Ser	Val	Gly	Val	Met	Leu	Tyr	Ile	
	475					480					485					
TTC	CTC	GCC	GGC	GTG	CCT	CCC	TTC	TGG	GCA	GAG	AAC	GAG	AAC	GGC	ATC	479
Phe	Leu	Ala	Gly	Val	Pro	Pro	Phe	Trp	Ala	Glu	Asn	Glu	Asn	Gly	Ile	
490					495					500					505	
TTC	ACC	GCC	ATC	CTG	CGA	GGG	CAG	CTT	GAC	CTC	TCC	AGC	GAG	CCA	TGG	527
Phe	Thr	Ala	Ile	Leu	Arg	Gly	Gln	Leu	Asp	Leu	Ser	Ser	Glu	Pro	Trp	
				510					515					520		
CCA	CAC	ATC	TCG	CCG	GGA	GCC	AAG	GAT	CTC	GTC	AAG	AAG	ATG	CTC	AAC	575
Pro	His	Ile	Ser	Pro	Gly	Ala	Lys	Asp	Leu	Val	Lys	Lys	Met	Leu	Asn	
			525					530					535			
ATC	AAC	CCC	AAG	GAG	CGG	CTC	ACG	GCG	TTC	CAG	GTC	CTC	AAT	CAC	CCA	623
Ile	Asn	Pro	Lys	Glu	Arg	Leu	Thr	Ala	Phe	Gln	Val		Asn	His	Pro	
		540					545					550				
TGG	ATC	AAA	GAA	GAC	GGA	GAC	GCG	CCT	GAC	ACG	CCG	CTT	GAC	AAC	GTT	671
Trp	Ile	Lys	Glu	Asp	Gly	Asp	Ala	Pro	Asp	Thr	Pro	Leu	Asp	Asn	Val	
	555					560					565					
GTT	CTC	GAC	AGG	CTC	AAG	CAG	TTC	AGG	GCC	ATG	AAC	CAG	TTC	AAG	AAA	719
Val	Leu	Asp	Arg	Leu	Lys	Gln	Phe	Arg	Ala	Met	Asn	Gln	Phe	Lys	Lys	
570					575					580					585	
GCA	GCA	TTG	AGG	ATC	ATA	GCT	GGG	TGC	CTA	TCC	GAA	GAG	GAG	ATC	ACA	767
Ala	Ala	Leu	Arg	Ile	Ile	Ala	Gly	Cys	Leu	Ser	Glu	Glu	Glu	Ile	Thr	
				590					595					600		
GGG	CTG	AAG	GAG	ATG	TTC	AAG	AAC	ATT	GAC	AAG	GAT	AAC	AGC	GGG	ACC	815
Gly	Leu	Lys	Glu	Met	Phe	Lys	Asn	Ile	Asp	Lys	Asp	Asn	Ser	Gly	Thr	
		605						610					615			
ATT	ACC	CTC	GAC	GAG	CTC	AAA	CAC	GGG	TTG	GCA	AAG	CAC	GGG	CCC	AAG	863
Ile	Thr	Leu	Asp	Glu	Leu	Lys	His	Gly	Leu	Ala	Lys	His	Gly	Pro	Lys	
		620					625					630				
CTG	TCA	GAC	AGC	GAA	ATG	GAG	AAA	CTA	ATG	GAA	GCA	GCT	GAC	GCT	GAC	911
Leu	Ser	Asp	Ser	Glu	Met	Glu	Lys	Leu	Met	Glu	Ala	Ala	Asp	Ala	Asp	
		635				640					645					
GGC	AAC	GGG	TTA	ATT	GAC	TAC	GAC	GAA	TTC	GTC	ACC	GCA	ACA	GTG	CAT	959
Gly	Asn	Gly	Leu	Ile	Asp	Tyr	Asp	Glu	Phe	Val	Thr	Ala	Thr	Val	His	
650					655					660					665	
ATG	AAC	AAA	CTG	GAT	AGA	GAA	GAG	CAC	CTT	TAC	ACA	GCA	TTC	CAG	TAT	1007
Met	Asn	Lys	Leu	Asp	Arg	Glu	Glu	His	Leu	Tyr	Thr	Ala	Phe	Gln	Tyr	
			670					675						680		
TTC	GAC	AAG	GAC	AAC	AGC	GGG	TAC	ATT	ACT	AAA	GAA	GAG	CTT	GAG	CAC	1055
Phe	Asp	Lys	Asp	Asn	Ser	Gly	Tyr	Ile	Thr	Lys	Glu	Glu	Leu	Glu	His	

685	690	695	
GCC TTG AAG GAG CAA GGG TTG TAT GAC GCC GAT AAA ATC AAA GAC ATC			1103
Ala Leu Lys Glu Gln Gly Leu Tyr Asp Ala Asp Lys Ile Lys Asp Ile			
700	705	710	
ATC TCC GAT GCC GAC TCT GAC AAT GAT GGA AGG ATA GAT TAT TCA GAG			1151
Ile Ser Asp Ala Asp Ser Asp Asn Asp Gly Arg Ile Asp Tyr Ser Glu			
715	720	725	
TTT GTG GCG ATG ATG AGG AAA GGG ACG GCT GGT GCC GAG CCA ATG AAC			1199
Phe Val Ala Met Met Arg Lys Gly Thr Ala Gly Ala Glu Pro Met Asn			
730	735	740	745
ATC AAG AAG AGG CGA GAC ATA GTC CTA TAGTGAAGTG AAGCAGCAAG			1246
Ile Lys Lys Arg Arg Asp Ile Val Leu			
750			
TGTGTAATGT AATGTGTATA GCAGCTCAAA CAAGCAAATT TGTACATCTG TACACAAATG			1306
CAATGGGGTT ACTTTTGCAA AAAAAAAAAA AAAAAAAAAA AAA			1349

(2) INFORMATION FOR SEQ ID NO:21:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 408 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:21:

Gln	Ile	Met	His	His	Leu	Ser	Gly	Gln	Pro	Asn	Val	Val	Gly	Leu	Arg
1				5					10					15	
Gly	Ala	Tyr	Glu	Asp	Lys	Gln	Ser	Val	His	Leu	Val	Met	Glu	Leu	Cys
			20					25					30		
Ala	Gly	Gly	Glu	Leu	Phe	Asp	Arg	Ile	Ile	Ala	Arg	Gly	Gln	Tyr	Thr
			35				40					45			
Glu	Arg	Gly	Ala	Ala	Glu	Leu	Leu	Arg	Ala	Ile	Val	Gln	Ile	Val	His
	50					55					60				
Thr	Cys	His	Ser	Met	Gly	Val	Met	His	Arg	Asp	Ile	Lys	Pro	Glu	Asn
65					70				75					80	
Phe	Leu	Leu	Leu	Ser	Lys	Asp	Glu	Asp	Ala	Pro	Leu	Lys	Ala	Thr	Asp
				85					90					95	
Phe	Gly	Leu	Ser	Val	Phe	Phe	Lys	Glu	Gly	Glu	Leu	Leu	Arg	Asp	Ile
			100					105					110		
Val	Gly	Ser	Ala	Tyr	Tyr	Ile	Ala	Pro	Glu	Val	Leu	Lys	Arg	Lys	Tyr
			115				120					125			
Gly	Pro	Glu	Ala	Asp	Ile	Trp	Ser	Val	Gly	Val	Met	Leu	Tyr	Ile	Phe
	130					135					140				

Leu Ala Gly Val Pro Pro Phe Trp Ala Glu Asn Glu Asn Gly Ile Phe
 145 150 155 160
 Thr Ala Ile Leu Arg Gly Gln Leu Asp Leu Ser Ser Glu Pro Trp Pro
 165 170 175
 His Ile Ser Pro Gly Ala Lys Asp Leu Val Lys Lys Met Leu Asn Ile
 180 185 190
 Asn Pro Lys Glu Arg Leu Thr Ala Phe Gln Val Leu Asn His Pro Trp
 195 200 205
 Ile Lys Glu Asp Gly Asp Ala Pro Asp Thr Pro Leu Asp Asn Val Val
 210 215 220
 Leu Asp Arg Leu Lys Gln Phe Arg Ala Met Asn Gln Phe Lys Lys Ala
 225 230 235 240
 Ala Leu Arg Ile Ile Ala Gly Cys Leu Ser Glu Glu Glu Ile Thr Gly
 245 250 255
 Leu Lys Glu Met Phe Lys Asn Ile Asp Lys Asp Asn Ser Gly Thr Ile
 260 265 270
 Thr Leu Asp Glu Leu Lys His Gly Leu Ala Lys His Gly Pro Lys Leu
 275 280 285
 Ser Asp Ser Glu Met Glu Lys Leu Met Glu Ala Ala Asp Ala Asp Gly
 290 295 300
 Asn Gly Leu Ile Asp Tyr Asp Glu Phe Val Thr Ala Thr Val His Met
 305 310 315 320
 Asn Lys Leu Asp Arg Glu Glu His Leu Tyr Thr Ala Phe Gln Tyr Phe
 325 330 335
 Asp Lys Asp Asn Ser Gly Tyr Ile Thr Lys Glu Glu Leu Glu His Ala
 340 345 350
 Leu Lys Glu Gln Gly Leu Tyr Asp Ala Asp Lys Ile Lys Asp Ile Ile
 355 360 365
 Ser Asp Ala Asp Ser Asp Asn Asp Gly Arg Ile Asp Tyr Ser Glu Phe
 370 375 380
 Val Ala Met Met Arg Lys Gly Thr Ala Gly Ala Glu Pro Met Asn Ile
 385 390 395 400
 Lys Lys Arg Arg Asp Ile Val Leu
 405

(2) INFORMATION FOR SEQ ID NO:22:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 464 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: NO

(ix) FEATURE:

(A) NAME/KEY: Protein
(B) LOCATION: 1..464
(D) OTHER INFORMATION: /note= "derived protein sequence of pollen specific CDPK as disclosed in Figure 34."

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:22:

Val Leu Gly Arg Pro Met Glu Asp Val Arg Ala Thr Tyr Ser Met Gly
1 5 10 15
Lys Glu Leu Gly Arg Gly Gln Phe Gly Val Thr His Leu Cys Thr His
20 25 30
Arg Thr Ser Gly Glu Lys Leu Ala Cys Lys Thr Ile Ala Lys Arg Lys
35 40 45
Leu Ala Ala Arg Glu Asp Val Asp Asp Val Arg Arg Glu Val Gln Ile
50 55 60
Met His His Leu Ser Gly Gln Pro Asn Val Val Gly Leu Arg Gly Ala
65 70 75 80
Tyr Glu Asp Lys Gln Ser Val His Leu Val Met Glu Leu Cys Ala Gly
85 90 95
Gly Glu Leu Phe Asp Arg Ile Ile Ala Arg Gly Gln Tyr Thr Glu Arg
100 105 110
Gly Ala Ala Glu Leu Leu Arg Ala Ile Val Gln Ile Val His Thr Cys
115 120 125
His Ser Met Gly Val Met His Arg Asp Ile Lys Pro Glu Asn Phe Leu
130 135 140
Leu Leu Ser Lys Asp Glu Asp Ala Pro Leu Lys Ala Thr Asp Phe Gly
145 150 155 160
Leu Ser Val Phe Phe Lys Glu Gly Glu Leu Leu Arg Asp Ile Val Gly
165 170 175
Ser Ala Tyr Tyr Ile Ala Pro Glu Val Leu Lys Arg Lys Tyr Gly Pro
180 185 190
Glu Ala Asp Ile Trp Ser Val Gly Val Met Leu Tyr Ile Phe Leu Ala
195 200 205
Gly Val Pro Pro Phe Trp Ala Glu Asn Glu Asn Gly Ile Phe Thr Ala
210 215 220
Ile Leu Arg Gly Gln Leu Asp Leu Ser Ser Glu Pro Trp Pro His Ile
225 230 235 240
Ser Pro Gly Ala Lys Asp Leu Val Lys Lys Met Leu Asn Ile Asn Pro
245 250 255
Lys Glu Arg Leu Thr Ala Phe Gln Val Leu Asn His Pro Trp Ile Lys

260							265					270				
Glu	Asp	Gly	Asp	Ala	Pro	Asp	Thr	Pro	Leu	Asp	Asn	Val	Val	Leu	Asp	
		275				280						285				
Arg	Leu	Lys	Gln	Phe	Arg	Ala	Met	Asn	Gln	Phe	Lys	Lys	Ala	Ala	Leu	
		290				295						300				
Arg	Ile	Ile	Ala	Gly	Cys	Leu	Ser	Glu	Glu	Glu	Ile	Thr	Gly	Leu	Lys	
305						310				315				320		
Glu	Met	Phe	Lys	Asn	Ile	Asp	Lys	Asp	Asn	Ser	Gly	Thr	Ile	Thr	Leu	
				325				330						335		
Asp	Glu	Leu	Lys	His	Gly	Leu	Ala	Lys	His	Gly	Pro	Lys	Leu	Ser	Asp	
		340						345				350				
Ser	Glu	Met	Glu	Lys	Leu	Met	Glu	Ala	Ala	Asp	Ala	Asp	Gly	Asn	Gly	
		355				360						365				
Leu	Ile	Asp	Tyr	Asp	Glu	Phe	Val	Thr	Ala	Thr	Val	His	Met	Asn	Lys	
370						375				380						
Leu	Asp	Arg	Glu	Glu	His	Leu	Tyr	Thr	Ala	Phe	Gln	Tyr	Phe	Asp	Lys	
385				390						395				400		
Asp	Asn	Ser	Gly	Tyr	Ile	Thr	Lys	Glu	Glu	Leu	Glu	His	Ala	Leu	Lys	
				405				410						415		
Glu	Gln	Gly	Leu	Tyr	Asp	Ala	Asp	Lys	Ile	Lys	Asp	Ile	Ile	Ser	Asp	
		420						425				430				
Ala	Asp	Ser	Asp	Asn	Asp	Gly	Arg	Ile	Asp	Tyr	Ser	Glu	Phe	Val	Ala	
		435				440						445				
Met	Met	Arg	Lys	Gly	Thr	Ala	Gly	Ala	Glu	Pro	Met	Asn	Ile	Lys	Lys	
450						455				460						

(2) INFORMATION FOR SEQ ID NO:23:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 295 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: NO

(ix) FEATURE:

- (A) NAME/KEY: Protein
(B) LOCATION: 1..295
(D) OTHER INFORMATION: /note= "rat protein kinase II
protein sequence as shown in Figure 32."

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:23:

Tyr Gln Leu Phe Glu Glu Leu Gly Lys Gly Ala Phe Ser Val Val Arg
 1 5 10 15
 Arg Cys Val Lys Lys Thr Ser Thr Gln Glu Tyr Ala Ala Lys Ile Ile
 20 25 30
 Asn Thr Lys Lys Leu Ser Ala Arg Asp His Gln Lys Leu Glu Arg Glu
 35 40 45
 Ala Arg Ile Cys Arg Leu Leu Lys His Pro Asn Ile Val Arg Leu His
 50 55 60
 Asp Ser Ile Ser Glu Glu Gly Phe His Tyr Leu Val Phe Asp Leu Val
 65 70 75 80
 Thr Gly Gly Glu Leu Phe Glu Asp Ile Val Ala Arg Glu Tyr Tyr Ser
 85 90 95
 Glu Ala Asp Ala Ser His Cys Ile His Gln Ile Leu Glu Ser Val Asn
 100 105 110
 His Ile His Gln His Asp Ile Val His Arg Asp Leu Lys Pro Glu Asn
 115 120 125
 Leu Leu Leu Ala Ser Lys Cys Lys Gly Ala Ala Val Lys Leu Ala Asp
 130 135 140
 Phe Gly Leu Ala Ile Glu Val Gln Gly Glu Gln Gln Ala Trp Phe Gly
 145 150 155 160
 Phe Ala Gly Thr Pro Gly Tyr Leu Ser Pro Glu Val Leu Arg Lys Asp
 165 170 175
 Pro Tyr Gly Lys Pro Val Asp Ile Trp Ala Cys Gly Val Ile Leu Tyr
 180 185 190
 Ile Leu Leu Val Gly Tyr Pro Pro Phe Trp Asp Glu Asp Gln His Lys
 195 200 205
 Leu Tyr Gln Gln Ile Lys Ala Gly Ala Tyr Asp Phe Pro Ser Pro Glu
 210 215 220
 Trp Asp Thr Val Thr Pro Glu Ala Lys Asn Leu Ile Asn Gln Met Leu
 225 230 235 240
 Thr Ile Asn Pro Ala Lys Arg Ile Thr Ala Asp Gln Ala Leu Lys His
 245 250 255
 Pro Trp Val Cys Gln Arg Ser Thr Val Ala Ser Met Met His Arg Gln
 260 265 270
 Glu Thr Val Glu Cys Leu Arg Lys Phe Asn Ala Arg Arg Lys Leu Lys
 275 280 285
 Gly Ala Ile Leu Thr Thr Met
 290 295

(2) INFORMATION FOR SEQ ID NO:24:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 142 amino acids

(B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: NO

(ix) FEATURE:

(A) NAME/KEY: Protein
 (B) LOCATION: 1..142
 (D) OTHER INFORMATION: /note= "human calmodulin protein
 sequence as shown in Figure 33."

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:24:

Leu	Thr	Glu	Glu	Gln	Ile	Ala	Glu	Phe	Lys	Glu	Ala	Phe	Ser	Leu	Phe	1	5	10	15
Asp	Lys	Asp	Gly	Asp	Gly	Thr	Ile	Thr	Thr	Lys	Glu	Leu	Gly	Thr	Val	20	25	30	
Met	Arg	Ser	Leu	Gly	Gln	Asn	Pro	Thr	Glu	Ala	Glu	Leu	Gln	Asp	Met	35	40	45	
Ile	Asn	Glu	Val	Asp	Ala	Asp	Gly	Asn	Gly	Thr	Ile	Asp	Phe	Pro	Glu	50	55	60	
Phe	Leu	Thr	Met	Met	Ala	Arg	Lys	Met	Lys	Asp	Thr	Asp	Ser	Glu	Glu	65	70	75	80
Glu	Ile	Arg	Glu	Ala	Phe	Arg	Val	Lys	Asp	Lys	Asp	Gly	Asn	Gly	Tyr	85	90	95	
Ile	Ser	Ala	Ala	Glu	Leu	Arg	His	Val	Met	Thr	Asn	Leu	Gly	Glu	Lys	100	105	110	
Leu	Thr	Asp	Glu	Glu	Val	Asp	Glu	Met	Ile	Arg	Glu	Ala	Asp	Ile	Asp	115	120	125	
Gly	Asp	Gly	Gln	Val	Asn	Tyr	Glu	Glu	Phe	Val	Gln	Met	Met	130	135	140			

(2) INFORMATION FOR SEQ ID NO:25:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 463 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: NO

(ix) FEATURE:

(A) NAME/KEY: Protein
 (B) LOCATION: 1..463

(D) OTHER INFORMATION: /note= "protein sequence for soybean CDPK as shown in Figure 34."

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:25:

```

Val Leu Pro Gln Arg Thr Gln Asn Ile Arg Glu Val Tyr Glu Val Gly
1          5          10          15
Arg Lys Leu Gly Gln Gly Gln Phe Gly Thr Thr Phe Glu Cys Thr Arg
20          25          30
Arg Ala Ser Gly Gly Lys Phe Ala Cys Lys Ser Ile Pro Lys Arg Lys
35          40          45
Leu Leu Cys Lys Glu Asp Tyr Glu Asp Val Trp Arg Glu Ile Gln Ile
50          55          60
Met His His Leu Ser Glu His Ala Asn Val Val Arg Ile Glu Gly Thr
65          70          75          80
Tyr Glu Asp Ser Thr Ala Val His Leu Val Met Glu Leu Cys Glu Gly
85          90          95
Gly Glu Leu Phe Asp Arg Ile Val Gln Lys Gly His Tyr Ser Glu Arg
100         105         110
Gln Ala Ala Arg Leu Ile Lys Thr Ile Val Glu Val Val Glu Ala Cys
115         120         125
His Ser Leu Gly Val Met His Arg Asp Leu Lys Pro Glu Asn Phe Leu
130         135         140
Phe Asp Thr Ile Asp Glu Asp Ala Lys Leu Lys Ala Thr Asp Phe Gly
145         150         155         160
Leu Ser Val Phe Tyr Lys Pro Gly Glu Ser Phe Cys Asp Val Val Gly
165         170         175
Ser Pro Tyr Tyr Val Ala Pro Glu Val Leu Arg Lys Leu Tyr Gly Pro
180         185         190
Glu Ser Asp Val Trp Ser Ala Gly Val Ile Leu Tyr Ile Leu Leu Ser
195         200         205
Gly Val Pro Pro Phe Trp Ala Glu Ser Glu Pro Gly Ile Phe Arg Gln
210         215         220
Ile Leu Leu Gly Lys Leu Asp Phe His Ser Glu Pro Trp Pro Ser Ile
225         230         235         240
Ser Asp Ser Ala Lys Asp Leu Ile Arg Lys Met Leu Asp Gln Asn Pro
245         250         255
Lys Thr Arg Leu Thr Ala His Glu Val Leu Arg His Pro Trp Ile Val
260         265         270
Asp Asp Asn Ile Ala Pro Asp Lys Pro Leu Asp Ser Ala Val Leu Ser
275         280         285
Arg Leu Lys Gln Phe Ser Ala Met Asn Lys Leu Lys Lys Met Ala Leu

```


1. *Chlorophyll a* (Chl *a*) is the primary photosynthetic pigment in most plants and algae. It is a green pigment that absorbs light energy in the blue and red regions of the visible spectrum.

1. *Chlorophyll a* (Chl *a*) is the primary photosynthetic pigment in most plants and algae. It is a green pigment that absorbs light energy in the blue and red regions of the visible spectrum.

1. *Chlorophyll a* (Chl *a*) is the primary photosynthetic pigment in most plants and algae. It is a green pigment that absorbs light energy in the blue and red regions of the visible spectrum.

1. *Chlorophyll a* (Chl *a*) is the primary photosynthetic pigment in most plants and algae. It is a green pigment that absorbs light energy in the blue and red regions of the visible spectrum.

1. *Chlorophyll a* (Chl *a*) is the primary photosynthetic pigment in most plants and algae. It is a green pigment that absorbs light energy in the blue and red regions of the visible spectrum.

Figure 6

1. *Chlorophyll a* (Chl *a*) is the primary photosynthetic pigment in most plants and algae. It is a green pigment that absorbs light energy in the blue and red regions of the visible spectrum.

1. *Chlorophyll a* (Chl *a*) is the primary photosynthetic pigment in most plants and algae. It is a green pigment that absorbs light energy in the blue and red regions of the visible spectrum.

1. *Chlorophyll a* (Chl *a*) is the primary photosynthetic pigment in most plants and algae. It is a green pigment that absorbs light energy in the blue and red regions of the visible spectrum.

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Figure 6

1. *Chlorophyll a* (Chl *a*) is the primary photosynthetic pigment in most plants and algae. It is a green pigment that absorbs light energy in the blue and red regions of the visible spectrum.

TAAGCAAATT TAGGAAAGTT AAAAGCACAC AATTAGGCAC ATGTGAAAGA TGTGTATGGT	600
AAGTAAAAGA CTTATAAGGA AAAAGTGGGT GAATCCTCAA GATGTGGTGG TATATCCCAA	660
TGATATTAGA TGCCAGAATA TAGGGGGGAA ATCGATGTAT ACCATCTCTA CCAGGATACC	720
TGTGCGGACT GTGCAACTGA CACATGGACC ATGGTGTCTT CTTAGATTTG GTTATTAGCT	780
AATTGCGCTA CAACTTGTTT AAGGCTAGAC CAAATTAAAA AACTAATATT AAACATAAAA	840
AGTTAGGCAA ACTATAGTAA ATTATGCAGC GATCCAACAA CAAGCCATGT CTCGTGGGTC	900
ATGAGCCACG CGTCGGCCAT ACACCCACAT GATGTTTCCA TACGGATGGT CCTTATGCAA	960
TTTTGTCTGC AAAACACAAG CCTTAATACA GCCACGCGAC AATCATGGAA GTGGTCGTTT	1020
TAGGTCTCTA TCATGAAGTT CAGGGAAAAC GCATCAAATG TAATGCAGAG AAATGGTATT	1080
TCTTCTCTTG TAAATCAGGG AGAGGAGTAC CATCAGTACA GATTTCAGAAT CAGAATTCAG	1140
TCTTCCAACG ACAATAATCG CAGCATCTTG TAAAAATTTG CAGAAACTTC TGTTTGA	1200
GTAGCCCTGA CCTTTGCAAA TATTTGAAGT TGTGCCTGCT GACACAACCTT CAATCTGGAA	1260
GTGCTGTTGA TCAGTTTTC CAGAAACAGC AAGCAGCCTA TATATATCTG TCACGAGACA	1320
CCCTGCCGCC CTCTTCTTTC CCGCCATTCC CTCCCTACCC TTCAAATCT AGAAACCTTT	1380
TTTTTTCCTC CCGATACGCC CCTCCATCTC TCGCCGTTCA TGTCCGTGGC TGGCTGCCCT	1440
CCGTGGGAGC AGGCGGCCGC ACTCGTTCCC CGCCGCAGCC ATGGGCCAGT GCTGCTCCAA	1500
GGGCGCCGGA GAGGCCCCGC CACCGAGGCG CCAAACGGCA GGCGCCAAGC CGCGGGCGTC	1560
CGCGAACAAC GCCGACGGAC AACGGGCGTC GTCTCTGTC GCGGTGGCTG CTGCCGCTGC	1620
TGCTGCCGGT GGTGGTGGCG GCGGCACGAC GAAGCCGGCC TCACCCACCG GCGGCGCCAG	1680
GGCCAGCTCC GGCAGCAAAC CGGCGGCGGC CGTGGGCACG GTGCTGGGCC GGCCCATGGA	1740
GGACGTGCGC GCGACCTACT CGATGGGCAA GGAGCTCGGG CGCGGGCAGT TCGGCGTGAC	1800
GCACCTGTGC ACGCACCGGA CGAGCGGCGA GAAGCTGGCG TGCAAGACGA TCGGAAGCG	1860
GAAGCTGGCG GCCAGGGAGG ACGTGGACGA CGTGCGGCGG GAGGTGCAGA TCATGCACCA	1920
CCTCTCCGGC CAGCCCAACG TGGTGGGCCT CCGCGGCGCG TACGAGGACA AGCAGAGCGT	1980
GCACCTCGTC ATGGAGCTGT GCGCGGGCGG GGAGCTCTTC GACCGCATCA TCGCCCGGGG	2040
CCAGTACACG GAGCGCGGCG CCGCGGAGCT GCTGCGCGCC ATCGTGCAGA TCGTGCACAC	2100
CTGCCACTCC ATGGGGGTGA TGCACCGGGA CATCAAGCCC GAGAACTTCC TGCTGCTCAG	2160
CAAGGACGAG GACGCGCCGC TCAAGGCCAC CGACTTCGGC CTCTCCGTCT TCTTCAAGGA	2220
GGGCGAGCTG CTCAGGGACA TCGTCGGCAG CGCCTACTAC ATCGCGCCCG AGGTGCTCAA	2280
GAGGAAGTAC GGCCCGGAGG CCGACATCTG GAGCGTCGGC GTCATGCTCT ACATCTTCCT	2340

(2) INFORMATION FOR SEQ ID NO:27:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 3546 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

- (A) DESCRIPTION: /desc = "Synthetic DNA"

(iii) HYPOTHETICAL: NO

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1..3543
- (D) OTHER INFORMATION: /product= "Full-length, hybrid maize optimized heat stable cryIA(b)"
/note= "DNA sequence as disclosed in Figure 37 as contained in pCIB5515."

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:27:

ATG GAC AAC AAC CCC AAC ATC AAC GAG TGC ATC CCC TAC AAC TGC CTG	48
Met Asp Asn Asn Pro Asn Ile Asn Glu Cys Ile Pro Tyr Asn Cys Leu	
410 415 420	
AGC AAC CCC GAG GTG GAG GTG CTG GGC GGC GAG CGC ATC GAG ACC GGC	96
Ser Asn Pro Glu Val Glu Val Leu Gly Gly Glu Arg Ile Glu Thr Gly	
425 430 435 440	
TAC ACC CCC ATC GAC ATC AGC CTG AGC CTG ACC CAG TTC CTG CTG AGC	144
Tyr Thr Pro Ile Asp Ile Ser Leu Ser Leu Thr Gln Phe Leu Leu Ser	
445 450 455	
GAG TTC GTG CCC GGC GCC GGC TTC GTG CTG GGC CTG GTG GAC ATC ATC	192
Glu Phe Val Pro Gly Ala Gly Phe Val Leu Gly Leu Val Asp Ile Ile	
460 465 470	
TGG GGC ATC TTC GGC CCC AGC CAG TGG GAC GCC TTC CTG GTG CAG ATC	240
Trp Gly Ile Phe Gly Pro Ser Gln Trp Asp Ala Phe Leu Val Gln Ile	
475 480 485	
GAG CAG CTG ATC AAC CAG CGC ATC GAG GAG TTC GCC CGC AAC CAG GCC	288
Glu Gln Leu Ile Asn Gln Arg Ile Glu Glu Phe Ala Arg Asn Gln Ala	
490 495 500	
ATC AGC CGC CTG GAG GGC CTG AGC AAC CTG TAC CAA ATC TAC GCC GAG	336
Ile Ser Arg Leu Glu Gly Leu Ser Asn Leu Tyr Gln Ile Tyr Ala Glu	
505 510 515 520	
AGC TTC CGC GAG TGG GAG GCC GAC CCC ACC AAC CCC GCC CTG CGC GAG	384
Ser Phe Arg Glu Trp Glu Ala Asp Pro Thr Asn Pro Ala Leu Arg Glu	
525 530 535	
GAG ATG CGC ATC CAG TTC AAC GAC ATG AAC AGC GCC CTG ACC ACC GCC	432
Glu Met Arg Ile Gln Phe Asn Asp Met Asn Ser Ala Leu Thr Thr Ala	
540 545 550	

ATC	CCC	CTG	TTC	GCC	GTG	CAG	AAC	TAC	CAG	GTG	CCC	CTG	CTG	AGC	GTG	480
Ile	Pro	Leu	Phe	Ala	Val	Gln	Asn	Tyr	Gln	Val	Pro	Leu	Leu	Ser	Val	
		555					560					565				
TAC	GTG	CAG	GCC	GCC	AAC	CTG	CAC	CTG	AGC	GTG	CTG	CGC	GAC	GTC	AGC	528
Tyr	Val	Gln	Ala	Ala	Asn	Leu	His	Leu	Ser	Val	Leu	Arg	Asp	Val	Ser	
	570					575					580					
GTG	TTC	GGC	CAG	CGC	TGG	GGC	TTC	GAC	GCC	GCC	ACC	ATC	AAC	AGC	CGC	576
Val	Phe	Gly	Gln	Arg	Trp	Gly	Phe	Asp	Ala	Ala	Thr	Ile	Asn	Ser	Arg	
585					590				595						600	
TAC	AAC	GAC	CTG	ACC	CGC	CTG	ATC	GGC	AAC	TAC	ACC	GAC	CAC	GCC	GTG	624
Tyr	Asn	Asp	Leu	Thr	Arg	Leu	Ile	Gly	Asn	Tyr	Thr	Asp	His	Ala	Val	
			605						610					615		
CGC	TGG	TAC	AAC	ACC	GGC	CTG	GAG	CGC	GTG	TGG	GGT	CCC	GAC	AGC	CGC	672
Arg	Trp	Tyr	Asn	Thr	Gly	Leu	Glu	Arg	Val	Trp	Gly	Pro	Asp	Ser	Arg	
			620					625					630			
GAC	TGG	ATC	AGG	TAC	AAC	CAG	TTC	CGC	CGC	GAG	CTG	ACC	CTG	ACC	GTG	720
Asp	Trp	Ile	Arg	Tyr	Asn	Gln	Phe	Arg	Arg	Glu	Leu	Thr	Leu	Thr	Val	
		635					640					645				
CTG	GAC	ATC	GTG	AGC	CTG	TTC	CCC	AAC	TAC	GAC	AGC	CGC	ACC	TAC	CCC	768
Leu	Asp	Ile	Val	Ser	Leu	Phe	Pro	Asn	Tyr	Asp	Ser	Arg	Thr	Tyr	Pro	
	650					655					660					
ATC	CGC	ACC	GTG	AGC	CAG	CTG	ACC	CGC	GAG	ATT	TAC	ACC	AAC	CCC	GTG	816
Ile	Arg	Thr	Val	Ser	Gln	Leu	Thr	Arg	Glu	Ile	Tyr	Thr	Asn	Pro	Val	
665					670				675						680	
CTG	GAG	AAC	TTC	GAC	GGC	AGC	TTC	CGC	GGC	AGC	GCC	CAG	GGC	ATC	GAG	864
Leu	Glu	Asn	Phe	Asp	Gly	Ser	Phe	Arg	Gly	Ser	Ala	Gln	Gly	Ile	Glu	
				685					690					695		
GGC	AGC	ATC	CGC	AGC	CCC	CAC	CTG	ATG	GAC	ATC	CTG	AAC	AGC	ATC	ACC	912
Gly	Ser	Ile	Arg	Ser	Pro	His	Leu	Met	Asp	Ile	Leu	Asn	Ser	Ile	Thr	
			700					705					710			
ATC	TAC	ACC	GAC	GCC	CAC	CGC	GGC	GAG	TAC	TAC	TGG	AGC	GGC	CAC	CAG	960
Ile	Tyr	Thr	Asp	Ala	His	Arg	Gly	Glu	Tyr	Tyr	Trp	Ser	Gly	His	Gln	
		715					720					725				
ATC	ATG	GCC	AGC	CCC	GTC	GGC	TTC	AGC	GGC	CCC	GAG	TTC	ACC	TTC	CCC	1008
Ile	Met	Ala	Ser	Pro	Val	Gly	Phe	Ser	Gly	Pro	Glu	Phe	Thr	Phe	Pro	
	730					735					740					
CTG	TAC	GGC	ACC	ATG	GGC	AAC	GCT	GCA	CCT	CAG	CAG	CGC	ATC	GTG	GCA	1056
Leu	Tyr	Gly	Thr	Met	Gly	Asn	Ala	Ala	Pro	Gln	Gln	Arg	Ile	Val	Ala	
745					750				755						760	
CAG	CTG	GGC	CAG	GGA	GTG	TAC	CGC	ACC	CTG	AGC	AGC	ACC	CTG	TAC	CGT	1104
Gln	Leu	Gly	Gln	Gly	Val	Tyr	Arg	Thr	Leu	Ser	Ser	Thr	Leu	Tyr	Arg	
			765					770						775		
CGA	CCT	TTC	AAC	ATC	GGC	ATC	AAC	AAC	CAG	CAG	CTG	AGC	GTG	CTG	GAC	1152
Arg	Pro	Phe	Asn	Ile	Gly	Ile	Asn	Asn	Gln	Gln	Leu	Ser	Val	Leu	Asp	
			780					785					790			

GGC ACC GAG TTC GCC TAC GGC ACC AGC AGC AAC CTG CCC AGC GCC GTG Gly Thr Glu Phe Ala Tyr Gly Thr Ser Ser Asn Leu Pro Ser Ala Val 795 800 805	1200
TAC CGC AAG AGC GGC ACC GTG GAC AGC CTG GAC GAG ATC CCC CCT CAG Tyr Arg Lys Ser Gly Thr Val Asp Ser Leu Asp Glu Ile Pro Pro Gln 810 815 820	1248
AAC AAC AAC GTG CCA CCT CGA CAG GGC TTC AGC CAC CGT CTG AGC CAC Asn Asn Asn Val Pro Pro Arg Gln Gly Phe Ser His Arg Leu Ser His 825 830 835 840	1296
GTG AGC ATG TTC CGC AGT GGC TTC AGC AAC AGC AGC GTG AGC ATC ATC Val Ser Met Phe Arg Ser Gly Phe Ser Asn Ser Ser Val Ser Ile Ile 845 850 855	1344
CGT GCA CCT ATG TTC AGC TGG ATT CAC CGC AGT GCC GAG TTC AAC AAC Arg Ala Pro Met Phe Ser Trp Ile His Arg Ser Ala Glu Phe Asn Asn 860 865 870	1392
ATC ATC CCC AGC AGC CAG ATC ACC CAG ATC CCC CTG ACC AAG AGC ACC Ile Ile Pro Ser Ser Gln Ile Thr Gln Ile Pro Leu Thr Lys Ser Thr 875 880 885	1440
AAC CTG GGC AGC GGC ACC AGC GTG GTG AAG GGC CCC GGC TTC ACC GGC Asn Leu Gly Ser Gly Thr Ser Val Val Lys Gly Pro Gly Phe Thr Gly 890 895 900	1488
GGC GAC ATC CTG CGC CGC ACC AGC CCC GGC CAG ATC AGC ACC CTG CGC Gly Asp Ile Leu Arg Arg Thr Ser Pro Gly Gln Ile Ser Thr Leu Arg 905 910 915 920	1536
GTG AAC ATC ACC GCC CCC CTG AGC CAG CGC TAC CGC GTC CGC ATC CGC Val Asn Ile Thr Ala Pro Leu Ser Gln Arg Tyr Arg Val Arg Ile Arg 925 930 935	1584
TAC GCC AGC ACC ACC AAC CTG CAG TTC CAC ACC AGC ATC GAC GGC CGC Tyr Ala Ser Thr Thr Asn Leu Gln Phe His Thr Ser Ile Asp Gly Arg 940 945 950	1632
CCC ATC AAC CAG GGC AAC TTC AGC GCC ACC ATG AGC AGC GGC AGC AAC Pro Ile Asn Gln Gly Asn Phe Ser Ala Thr Met Ser Ser Gly Ser Asn 955 960 965	1680
CTG CAG AGC GGC AGC TTC CGC ACC GTG GGC TTC ACC ACC CCC TTC AAC Leu Gln Ser Gly Ser Phe Arg Thr Val Gly Phe Thr Thr Pro Phe Asn 970 975 980	1728
TTC AGC AAC GGC AGC AGC GTG TTC ACC CTG AGC GCC CAC GTG TTC AAC Phe Ser Asn Gly Ser Ser Val Phe Thr Leu Ser Ala His Val Phe Asn 985 990 995 1000	1776
AGC GGC AAC GAG GTG TAC ATC GAC CGC ATC GAG TTC GTG CCC GCC GAG Ser Gly Asn Glu Val Tyr Ile Asp Arg Ile Glu Phe Val Pro Ala Glu 1005 1010 1015	1824
GTG ACC TTC GAG GCC GAG TAC GAC CTG GAG AGG GCT CAG AAG GCC GTG Val Thr Phe Glu Ala Glu Tyr Asp Leu Glu Arg Ala Gln Lys Ala Val 1020 1025 1030	1872
AAC GAG CTG TTC ACC AGC AGC AAC CAG ATC GGC CTG AAG ACC GAC GTG	1920

Asn	Glu	Leu	Phe	Thr	Ser	Ser	Asn	Gln	Ile	Gly	Leu	Lys	Thr	Asp	Val	
		1035						1040					1045			
ACC	GAC	TAC	CAC	ATC	GAT	CAA	GTA	TCC	AAT	TTA	GTT	GAG	TGT	TTA	TCT	1968
Thr	Asp	Tyr	His	Ile	Asp	Gln	Val	Ser	Asn	Leu	Val	Glu	Cys	Leu	Ser	
		1050					1055				1060					
GAT	GAA	TTT	TGT	CTG	GAT	GAA	AAA	AAA	GAA	TTG	TCC	GAG	AAA	GTC	AAA	2016
Asp	Glu	Phe	Cys	Leu	Asp	Glu	Lys	Lys	Glu	Leu	Ser	Glu	Lys	Val	Lys	
		1065					1070				1075				1080	
CAT	GCG	AAG	CGA	CTT	AGT	GAT	GAG	CGG	AAT	TTA	CTT	CAA	GAT	CCA	AAC	2064
His	Ala	Lys	Arg	Leu	Ser	Asp	Glu	Arg	Asn	Leu	Leu	Gln	Asp	Pro	Asn	
					1085					1090					1095	
TTT	AGA	GGG	ATC	AAT	AGA	CAA	CTA	GAC	CGT	GGC	TGG	AGA	GGA	AGT	ACG	2112
Phe	Arg	Gly	Ile	Asn	Arg	Gln	Leu	Asp	Arg	Gly	Trp	Arg	Gly	Ser	Thr	
			1100						1105					1110		
GAT	ATT	ACC	ATC	CAA	GGA	GGC	GAT	GAC	GTA	TTC	AAA	GAG	AAT	TAC	GTT	2160
Asp	Ile	Thr	Ile	Gln	Gly	Gly	Asp	Asp	Val	Phe	Lys	Glu	Asn	Tyr	Val	
			1115					1120					1125			
ACG	CTA	TTG	GGT	ACC	TTT	GAT	GAG	TGC	TAT	CCA	ACG	TAT	TTA	TAT	CAA	2208
Thr	Leu	Leu	Gly	Thr	Phe	Asp	Glu	Cys	Tyr	Pro	Thr	Tyr	Leu	Tyr	Gln	
		1130					1135					1140				
AAA	ATA	GAT	GAG	TCG	AAA	TTA	AAA	GCC	TAT	ACC	CGT	TAC	CAA	TTA	AGA	2256
Lys	Ile	Asp	Glu	Ser	Lys	Leu	Lys	Ala	Tyr	Thr	Arg	Tyr	Gln	Leu	Arg	
		1145					1150				1155				1160	
GGG	TAT	ATC	GAA	GAT	AGT	CAA	GAC	TTA	GAA	ATC	TAT	TTA	ATT	CGC	TAC	2304
Gly	Tyr	Ile	Glu	Asp	Ser	Gln	Asp	Leu	Glu	Ile	Tyr	Leu	Ile	Arg	Tyr	
					1165					1170					1175	
AAT	GCC	AAA	CAC	GAA	ACA	GTA	AAT	GTG	CCA	GGT	ACG	GGT	TCC	TTA	TGG	2352
Asn	Ala	Lys	His	Glu	Thr	Val	Asn	Val	Pro	Gly	Thr	Gly	Ser	Leu	Trp	
					1180				1185					1190		
CCG	CTT	TCA	GCC	CCA	AGT	CCA	ATC	GGA	AAA	TGT	GGG	GAG	CCG	AAT	CGA	2400
Pro	Leu	Ser	Ala	Pro	Ser	Pro	Ile	Gly	Lys	Cys	Gly	Glu	Pro	Asn	Arg	
			1195					1200					1205			
TGC	GCT	CCG	CAC	CTG	GAG	TGG	AAC	CCG	GAC	CTA	GAC	TGC	AGC	TGC	AGG	2448
Cys	Ala	Pro	His	Leu	Glu	Trp	Asn	Pro	Asp	Leu	Asp	Cys	Ser	Cys	Arg	
		1210					1215					1220				
GAC	GGG	GAG	AAG	TGC	GCC	CAT	CAT	TCC	CAT	CAT	TTC	TCC	TTG	GAC	ATT	2496
Asp	Gly	Glu	Lys	Cys	Ala	His	His	Ser	His	His	Phe	Ser	Leu	Asp	Ile	
		1225				1230					1235				1240	
GAT	GTT	GGA	TGT	ACA	GAC	TTA	AAT	GAG	GAC	TTA	GGT	GTA	TGG	GTG	ATA	2544
Asp	Val	Gly	Cys	Thr	Asp	Leu	Asn	Glu	Asp	Leu	Gly	Val	Trp	Val	Ile	
					1245					1250					1255	
TTC	AAG	ATT	AAG	ACG	CAA	GAT	GGC	CAT	GCA	AGA	CTA	GGA	AAT	CTA	GAA	2592
Phe	Lys	Ile	Lys	Thr	Gln	Asp	Gly	His	Ala	Arg	Leu	Gly	Asn	Leu	Glu	
				1260					1265					1270		
TTT	CTC	GAA	GAG	AAA	CCA	TTA	GTA	GGA	GAA	GCA	CTA	GCT	CGT	GTG	AAA	2640
Phe	Leu	Glu	Glu	Lys	Pro	Leu	Val	Gly	Glu	Ala	Leu	Ala	Arg	Val	Lys	

1275	1280	1285	
AGA GCG GAG AAA AAA TGG	AGA GAC AAA CGT GAA AAA TTG GAA TGG GAA	2688	
Arg Ala Glu Lys Lys Trp	Arg Asp Lys Arg Glu Lys Leu Glu Trp Glu		
1290	1295	1300	
ACA AAT ATT GTT TAT AAA GAG GCA AAA GAA TCT GTA GAT GCT TTA TTT	2736		
Thr Asn Ile Val Tyr Lys Glu Ala Lys Glu Ser Val Asp Ala Leu Phe			
1305	1310	1315	1320
GTA AAC TCT CAA TAT GAT AGA TTA CAA GCG GAT ACC AAC ATC GCG ATG	2784		
Val Asn Ser Gln Tyr Asp Arg Leu Gln Ala Asp Thr Asn Ile Ala Met			
1325	1330	1335	
ATT CAT GCG GCA GAT AAA CGC GTT CAT AGC ATT CGA GAA GCT TAT CTG	2832		
Ile His Ala Ala Asp Lys Arg Val His Ser Ile Arg Glu Ala Tyr Leu			
1340	1345	1350	
CCT GAG CTG TCT GTG ATT CCG GGT GTC AAT GCG GCT ATT TTT GAA GAA	2880		
Pro Glu Leu Ser Val Ile Pro Gly Val Asn Ala Ala Ile Phe Glu Glu			
1355	1360	1365	
TTA GAA GGG CGT ATT TTC ACT GCA TTC TCC CTA TAT GAT GCG AGA AAT	2928		
Leu Glu Gly Arg Ile Phe Thr Ala Phe Ser Leu Tyr Asp Ala Arg Asn			
1370	1375	1380	
GTC ATT AAA AAT GGT GAT TTT AAT AAT GGC TTA TCC TGC TGG AAC GTG	2976		
Val Ile Lys Asn Gly Asp Phe Asn Asn Gly Leu Ser Cys Trp Asn Val			
1385	1390	1395	1400
AAA GGG CAT GTA GAT GTA GAA GAA CAA AAC AAC CAC CGT TCG GTC CTT	3024		
Lys Gly His Val Asp Val Glu Glu Gln Asn Asn His Arg Ser Val Leu			
1405	1410	1415	
GTT GTT CCG GAA TGG GAA GCA GAA GTG TCA CAA GAA GTT CGT GTC TGT	3072		
Val Val Pro Glu Trp Glu Ala Glu Val Ser Gln Glu Val Arg Val Cys			
1420	1425	1430	
CCG GGT CGT GGC TAT ATC CTT CGT GTC ACA GCG TAC AAG GAG GGA TAT	3120		
Pro Gly Arg Gly Tyr Ile Leu Arg Val Thr Ala Tyr Lys Glu Gly Tyr			
1435	1440	1445	
GGA GAA GGT TGC GTA ACC ATT CAT GAG ATC GAG AAC AAT ACA GAC GAA	3168		
Gly Glu Gly Cys Val Thr Ile His Glu Ile Glu Asn Asn Thr Asp Glu			
1450	1455	1460	
CTG AAG TTT AGC AAC TGT GTA GAA GAG GAA GTA TAT CCA AAC AAC ACG	3216		
Leu Lys Phe Ser Asn Cys Val Glu Glu Glu Val Tyr Pro Asn Asn Thr			
1465	1470	1475	1480
GTA ACG TGT AAT GAT TAT ACT GCG ACT CAA GAA GAA TAT GAG GGT ACG	3264		
Val Thr Cys Asn Asp Tyr Thr Ala Thr Gln Glu Glu Tyr Glu Gly Thr			
1485	1490	1495	
TAC ACT TCT CGT AAT CGA GGA TAT GAC GGA GCC TAT GAA AGC AAT TCT	3312		
Tyr Thr Ser Arg Asn Arg Gly Tyr Asp Gly Ala Tyr Glu Ser Asn Ser			
1500	1505	1510	
TCT GTA CCA GCT GAT TAT GCA TCA GCC TAT GAA GAA AAA GCA TAT ACA	3360		
Ser Val Pro Ala Asp Tyr Ala Ser Ala Tyr Glu Glu Lys Ala Tyr Thr			
1515	1520	1525	

GAT GGA CGA AGA GAC AAT CCT TGT GAA TCT AAC AGA GGA TAT GGG GAT	3438
Asp Gly Arg Arg Asp Asn Pro Cys Glu Ser Asn Arg Gly Tyr Gly Asp	
1530 1535 1540	
TAC ACA CCA CTA CCA GCT GGC TAT GTG ACA AAA GAA TTA GAG TAC TTC	3456
Tyr Thr Pro Leu Pro Ala Gly Tyr Val Thr Lys Glu Leu Glu Tyr Phe	
1545 1550 1555 1560	
CCA GAA ACC GAT AAG GTA TGG ATT GAG ATC GGA GAA ACG GAA GGA ACA	3504
Pro Glu Thr Asp Lys Val Trp Ile Glu Ile Gly Glu Thr Glu Gly Thr	
1565 1570 1575	
TTC ATC GTG GAC AGC GTG GAA TTA CTT CTT ATG GAG GAA TAA	3546
Phe Ile Val Asp Ser Val Glu Leu Leu Leu Met Glu Glu	
1580 1585	

(2) INFORMATION FOR SEQ ID NO:28:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1181 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:28:

Met	Asp	Asn	Asn	Pro	Asn	Ile	Asn	Glu	Cys	Ile	Pro	Tyr	Asn	Cys	Leu
1				5				10						15	
Ser	Asn	Pro	Glu	Val	Glu	Val	Leu	Gly	Gly	Glu	Arg	Ile	Glu	Thr	Gly
			20					25					30		
Tyr	Thr	Pro	Ile	Asp	Ile	Ser	Leu	Ser	Leu	Thr	Gln	Phe	Leu	Leu	Ser
			35				40					45			
Glu	Phe	Val	Pro	Gly	Ala	Gly	Phe	Val	Leu	Gly	Leu	Val	Asp	Ile	Ile
		50				55					60				
Trp	Gly	Ile	Phe	Gly	Pro	Ser	Gln	Trp	Asp	Ala	Phe	Leu	Val	Gln	Ile
	65				70				75					80	
Glu	Gln	Leu	Ile	Asn	Gln	Arg	Ile	Glu	Glu	Phe	Ala	Arg	Asn	Gln	Ala
				85				90						95	
Ile	Ser	Arg	Leu	Glu	Gly	Leu	Ser	Asn	Leu	Tyr	Gln	Ile	Tyr	Ala	Glu
			100					105					110		
Ser	Phe	Arg	Glu	Trp	Glu	Ala	Asp	Pro	Thr	Asn	Pro	Ala	Leu	Arg	Glu
		115					120					125			
Glu	Met	Arg	Ile	Gln	Phe	Asn	Asp	Met	Asn	Ser	Ala	Leu	Thr	Thr	Ala
	130					135					140				
Ile	Pro	Leu	Phe	Ala	Val	Gln	Asn	Tyr	Gln	Val	Pro	Leu	Leu	Ser	Val
	145				150				155					160	
Tyr	Val	Gln	Ala	Ala	Asn	Leu	His	Leu	Ser	Val	Leu	Arg	Asp	Val	Ser
				165				170						175	

Val Phe Gly Gln Arg Trp Gly Phe Asp Ala Ala Thr Ile Asn Ser Arg
180 185 190
Tyr Asn Asp Leu Thr Arg Leu Ile Gly Asn Tyr Thr Asp His Ala Val
195 200 205
Arg Trp Tyr Asn Thr Gly Leu Glu Arg Val Trp Gly Pro Asp Ser Arg
210 215 220
Asp Trp Ile Arg Tyr Asn Gln Phe Arg Arg Glu Leu Thr Leu Thr Val
225 230 235 240
Leu Asp Ile Val Ser Leu Phe Pro Asn Tyr Asp Ser Arg Thr Tyr Pro
245 250 255
Ile Arg Thr Val Ser Gln Leu Thr Arg Glu Ile Tyr Thr Asn Pro Val
260 265 270
Leu Glu Asn Phe Asp Gly Ser Phe Arg Gly Ser Ala Gln Gly Ile Glu
275 280 285
Gly Ser Ile Arg Ser Pro His Leu Met Asp Ile Leu Asn Ser Ile Thr
290 295 300
Ile Tyr Thr Asp Ala His Arg Gly Glu Tyr Tyr Trp Ser Gly His Gln
305 310 315 320
Ile Met Ala Ser Pro Val Gly Phe Ser Gly Pro Glu Phe Thr Phe Pro
325 330 335
Leu Tyr Gly Thr Met Gly Asn Ala Ala Pro Gln Gln Arg Ile Val Ala
340 345 350
Gln Leu Gly Gln Gly Val Tyr Arg Thr Leu Ser Ser Thr Leu Tyr Arg
355 360 365
Arg Pro Phe Asn Ile Gly Ile Asn Asn Gln Gln Leu Ser Val Leu Asp
370 375 380
Gly Thr Glu Phe Ala Tyr Gly Thr Ser Ser Asn Leu Pro Ser Ala Val
385 390 395 400
Tyr Arg Lys Ser Gly Thr Val Asp Ser Leu Asp Glu Ile Pro Pro Gln
405 410 415
Asn Asn Asn Val Pro Pro Arg Gln Gly Phe Ser His Arg Leu Ser His
420 425 430
Val Ser Met Phe Arg Ser Gly Phe Ser Asn Ser Ser Val Ser Ile Ile
435 440 445
Arg Ala Pro Met Phe Ser Trp Ile His Arg Ser Ala Glu Phe Asn Asn
450 455 460
Ile Ile Pro Ser Ser Gln Ile Thr Gln Ile Pro Leu Thr Lys Ser Thr
465 470 475 480
Asn Leu Gly Ser Gly Thr Ser Val Val Lys Gly Pro Gly Phe Thr Gly
485 490 495

Gly	Asp	Ile	Leu	Arg	Arg	Thr	Ser	Pro	Gly	Gln	Ile	Ser	Thr	Leu	Arg
			500					505					510		
Val	Asn	Ile	Thr	Ala	Pro	Leu	Ser	Gln	Arg	Tyr	Arg	Val	Arg	Ile	Arg
			515				520					525			
Tyr	Ala	Ser	Thr	Thr	Asn	Leu	Gln	Phe	His	Thr	Ser	Ile	Asp	Gly	Arg
			530				535				540				
Pro	Ile	Asn	Gln	Gly	Asn	Phe	Ser	Ala	Thr	Met	Ser	Ser	Gly	Ser	Asn
			545				550				555				560
Leu	Gln	Ser	Gly	Ser	Phe	Arg	Thr	Val	Gly	Phe	Thr	Thr	Pro	Phe	Asn
				565					570					575	
Phe	Ser	Asn	Gly	Ser	Ser	Val	Phe	Thr	Leu	Ser	Ala	His	Val	Phe	Asn
			580					585					590		
Ser	Gly	Asn	Glu	Val	Tyr	Ile	Asp	Arg	Ile	Glu	Phe	Val	Pro	Ala	Glu
			595				600					605			
Val	Thr	Phe	Glu	Ala	Glu	Tyr	Asp	Leu	Glu	Arg	Ala	Gln	Lys	Ala	Val
			610				615					620			
Asn	Glu	Leu	Phe	Thr	Ser	Ser	Asn	Gln	Ile	Gly	Leu	Lys	Thr	Asp	Val
			625				630				635				640
Thr	Asp	Tyr	His	Ile	Asp	Gln	Val	Ser	Asn	Leu	Val	Glu	Cys	Leu	Ser
				645					650					655	
Asp	Glu	Phe	Cys	Leu	Asp	Glu	Lys	Lys	Glu	Leu	Ser	Glu	Lys	Val	Lys
			660					665					670		
His	Ala	Lys	Arg	Leu	Ser	Asp	Glu	Arg	Asn	Leu	Leu	Gln	Asp	Pro	Asn
			675				680					685			
Phe	Arg	Gly	Ile	Asn	Arg	Gln	Leu	Asp	Arg	Gly	Trp	Arg	Gly	Ser	Thr
			690				695					700			
Asp	Ile	Thr	Ile	Gln	Gly	Gly	Asp	Asp	Val	Phe	Lys	Glu	Asn	Tyr	Val
			705				710				715				720
Thr	Leu	Leu	Gly	Thr	Phe	Asp	Glu	Cys	Tyr	Pro	Thr	Tyr	Leu	Tyr	Gln
				725					730					735	
Lys	Ile	Asp	Glu	Ser	Lys	Leu	Lys	Ala	Tyr	Thr	Arg	Tyr	Gln	Leu	Arg
			740					745					750		
Gly	Tyr	Ile	Glu	Asp	Ser	Gln	Asp	Leu	Glu	Ile	Tyr	Leu	Ile	Arg	Tyr
			755				760					765			
Asn	Ala	Lys	His	Glu	Thr	Val	Asn	Val	Pro	Gly	Thr	Gly	Ser	Leu	Trp
			770				775					780			
Pro	Leu	Ser	Ala	Pro	Ser	Pro	Ile	Gly	Lys	Cys	Gly	Glu	Pro	Asn	Arg
			785				790				795				800
Cys	Ala	Pro	His	Leu	Glu	Trp	Asn	Pro	Asp	Leu	Asp	Cys	Ser	Cys	Arg
				805					810					815	
Asp	Gly	Glu	Lys	Cys	Ala	His	His	Ser	His	His	Phe	Ser	Leu	Asp	Ile

820					825					830					
Asp	Val	Gly	Cys	Thr	Asp	Leu	Asn	Glu	Asp	Leu	Gly	Val	Trp	Val	Ile
		835					840					845			
Phe	Lys	Ile	Lys	Thr	Gln	Asp	Gly	His	Ala	Arg	Leu	Gly	Asn	Leu	Glu
	850					855					860				
Phe	Leu	Glu	Glu	Lys	Pro	Leu	Val	Gly	Glu	Ala	Leu	Ala	Arg	Val	Lys
	865					870					875				880
Arg	Ala	Glu	Lys	Lys	Trp	Arg	Asp	Lys	Arg	Glu	Lys	Leu	Glu	Trp	Glu
				885					890					895	
Thr	Asn	Ile	Val	Tyr	Lys	Glu	Ala	Lys	Glu	Ser	Val	Asp	Ala	Leu	Phe
			900					905					910		
Val	Asn	Ser	Gln	Tyr	Asp	Arg	Leu	Gln	Ala	Asp	Thr	Asn	Ile	Ala	Met
		915					920					925			
Ile	His	Ala	Ala	Asp	Lys	Arg	Val	His	Ser	Ile	Arg	Glu	Ala	Tyr	Leu
	930					935					940				
Pro	Glu	Leu	Ser	Val	Ile	Pro	Gly	Val	Asn	Ala	Ala	Ile	Phe	Glu	Glu
	945					950					955				960
Leu	Glu	Gly	Arg	Ile	Phe	Thr	Ala	Phe	Ser	Leu	Tyr	Asp	Ala	Arg	Asn
				965					970					975	
Val	Ile	Lys	Asn	Gly	Asp	Phe	Asn	Asn	Gly	Leu	Ser	Cys	Trp	Asn	Val
			980						985				990		
Lys	Gly	His	Val	Asp	Val	Glu	Glu	Gln	Asn	Asn	His	Arg	Ser	Val	Leu
		995					1000					1005			
Val	Val	Pro	Glu	Trp	Glu	Ala	Glu	Val	Ser	Gln	Glu	Val	Arg	Val	Cys
	1010					1015					1020				
Pro	Gly	Arg	Gly	Tyr	Ile	Leu	Arg	Val	Thr	Ala	Tyr	Lys	Glu	Gly	Tyr
	1025					1030					1035				1040
Gly	Glu	Gly	Cys	Val	Thr	Ile	His	Glu	Ile	Glu	Asn	Asn	Thr	Asp	Glu
				1045					1050					1055	
Leu	Lys	Phe	Ser	Asn	Cys	Val	Glu	Glu	Glu	Val	Tyr	Pro	Asn	Asn	Thr
			1060					1065					1070		
Val	Thr	Cys	Asn	Asp	Tyr	Thr	Ala	Thr	Gln	Glu	Glu	Tyr	Glu	Gly	Thr
		1075					1080						1085		
Tyr	Thr	Ser	Arg	Asn	Arg	Gly	Tyr	Asp	Gly	Ala	Tyr	Glu	Ser	Asn	Ser
	1090					1095					1100				
Ser	Val	Pro	Ala	Asp	Tyr	Ala	Ser	Ala	Tyr	Glu	Glu	Lys	Ala	Tyr	Thr
	1105					1110					1115				1120
Asp	Gly	Arg	Arg	Asp	Asn	Pro	Cys	Glu	Ser	Asn	Arg	Gly	Tyr	Gly	Asp
				1125					1130					1135	
Tyr	Thr	Pro	Leu	Pro	Ala	Gly	Tyr	Val	Thr	Lys	Glu	Leu	Glu	Tyr	Phe
			1140					1145					1150		

Pro Glu Thr Asp Lys Val Trp Ile Glu Ile Gly Glu Thr Glu Gly Thr
 1155 1160 1165

Phe Ile Val Asp Ser Val Glu Leu Leu Leu Met Glu Glu
 1170 1175 1180

(2) INFORMATION FOR SEQ ID NO:29:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 88 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: other nucleic acid
 - (A) DESCRIPTION: /desc = "primer KE74A28"

(iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:29:

GCAGATCTGG ATCCATGCAC GCCGTGAAGG GCCCTTCTAG AAGGCCTATC GATAAAGAGC	60
TCCCCGGGGA TGGATTGCAC GCAGGTTC	88

(2) INFORMATION FOR SEQ ID NO:30:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 40 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: other nucleic acid
 - (A) DESCRIPTION: /desc = "primer KE72A28"

(iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:30:

GCGTTAACAT GTCGACTCAG AAGAACTCGT CAAGAAGGCG	40
---	----

(2) INFORMATION FOR SEQ ID NO:31:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 22 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: other nucleic acid
 - (A) DESCRIPTION: /desc = "primer P1(a)"

(iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:31:

GTCGACAAGG ATCCAACAAT GG

22

(2) INFORMATION FOR SEQ ID NO:32:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 26 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(A) DESCRIPTION: /desc = "primer P1(b)"

(iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:32:

AATTGTCGAC AAGGATCCAA CAATGG

26

(2) INFORMATION FOR SEQ ID NO:33:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 23 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(A) DESCRIPTION: /desc = "primer P2(a)"

(iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:33:

ACACGCTGAC GTCGCGCAGC ACG

23

(2) INFORMATION FOR SEQ ID NO:34:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 23 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(A) DESCRIPTION: /desc = "primer P2(b)"

(iii) HYPOTHETICAL: NO

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO:37:

GCTGCGCGAC GTCAGCGTGT TCGG

24

(2) INFORMATION FOR SEQ ID NO:38:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 23 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(A) DESCRIPTION: /desc = "primer P3(b)"

(iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:38:

AATTGCTGCG CGACGTCAGC GTG

23

(2) INFORMATION FOR SEQ ID NO:39:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 25 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(A) DESCRIPTION: /desc = "primer P4(a)"

(iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:39:

GGCGTTGCCC ATGGTGCCGT ACAGG

25

(2) INFORMATION FOR SEQ ID NO:40:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 23 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(A) DESCRIPTION: /desc = "primer P4(b)"

(iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:40:

AGCTGGCGTT GCCCATGGTG CCG

23

(2) INFORMATION FOR SEQ ID NO:41:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 10 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(A) DESCRIPTION: /desc = "primer B1"

(iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:41:

AATTGCTGCG

10

(2) INFORMATION FOR SEQ ID NO:42:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 10 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(A) DESCRIPTION: /desc = "primer B2"

(iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:42:

AACGCCAGCT

10

(2) INFORMATION FOR SEQ ID NO:43:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 32 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(A) DESCRIPTION: /desc = "primer P5(a)"

(iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:43:

TTCCCCCTGT ACGGCACCAT GGGCAACGCC GC

32

(2) INFORMATION FOR SEQ ID NO:44:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 23 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(A) DESCRIPTION: /desc = "primer P5(b) "

(iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:44:

AATTGTACGG CACCATGGGC AAC

23

(2) INFORMATION FOR SEQ ID NO:45:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 26 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(A) DESCRIPTION: /desc = "primer P6(a) "

(iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:45:

GAAGCCGGGG CCCTTCACCA CGCTGG

26

(2) INFORMATION FOR SEQ ID NO:46:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 23 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(A) DESCRIPTION: /desc = "primer P6(b) "

(iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:46:

AGCTGAAGCC GGGGCCCTTC ACC

23

(2) INFORMATION FOR SEQ ID NO:47:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 10 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: other nucleic acid
 - (A) DESCRIPTION: /desc = "primer C1"
- (iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:47:

AATTGTACGG

10

(2) INFORMATION FOR SEQ ID NO:48:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 13 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: other nucleic acid
 - (A) DESCRIPTION: /desc = "primer C2 - first half"
- (iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:48:

TTCCCCTGTA CGG

13

(2) INFORMATION FOR SEQ ID NO:49:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 10 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: other nucleic acid
 - (A) DESCRIPTION: /desc = "primer C1 - second half"
- (iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:49:

GGCTTCAGCT

10

(2) INFORMATION FOR SEQ ID NO:50:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 19 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: other nucleic acid
 - (A) DESCRIPTION: /desc = "primer PEPCivs#9 - forward"
- (iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:50:

GTACAAAAAC CAGCAACTC

19

(2) INFORMATION FOR SEQ ID NO:51:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 19 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: other nucleic acid
 - (A) DESCRIPTION: /desc = "primer PEPCivs#9 reverse"
- (iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:51:

CTGCACAAAG TGGAGTAGT

19

(2) INFORMATION FOR SEQ ID NO:52:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 25 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: other nucleic acid
 - (A) DESCRIPTION: /desc = "primer P7(a)"
- (iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:52:

TGGTGAAGGG CCCCGGCTTC ACCGG

25

(2) INFORMATION FOR SEQ ID NO:53:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 36 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: other nucleic acid
 - (A) DESCRIPTION: /desc = "primer P8(a)"
- (iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:53:

ATCATCGATG AGCTCCTACA CCTGATCGAT GTGGTA

36

(2) INFORMATION FOR SEQ ID NO:54:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: other nucleic acid
 - (A) DESCRIPTION: /desc = "primer for fourth quarter - second half"
- (iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:54:

ATCAGGAGCT CATCGATGAT

20

(2) INFORMATION FOR SEQ ID NO:55:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 11 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: other nucleic acid
 - (A) DESCRIPTION: /desc = "primer for third quarter - first half"
- (iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:55:

TTCCCCCTGT A

11

(2) INFORMATION FOR SEQ ID NO:56:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: other nucleic acid
 - (A) DESCRIPTION: /desc = "primer MK23A28"
- (iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:56:

GGGGCTGCGG ATGCTGCCCT

20

(2) INFORMATION FOR SEQ ID NO:57:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: other nucleic acid
 - (A) DESCRIPTION: /desc = "primer MK25A28"
- (iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:57:

GAGCTGACCC TGACCGTGCT

20

(2) INFORMATION FOR SEQ ID NO:58:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: other nucleic acid
 - (A) DESCRIPTION: /desc = "primer MK26A28"
- (iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:58:

CACCTGATGG ACATCCTGAA

20

(2) INFORMATION FOR SEQ ID NO:59:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 33 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(A) DESCRIPTION: /desc = "sequence in pCIB3073 prior to deletion"

(iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:59:

TATAAGGATC CCGGGGGCAA GATCTGAGAT ATG

33

(2) INFORMATION FOR SEQ ID NO:60:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 44 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(A) DESCRIPTION: /desc = "primer KE134A28"

(iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:60:

CGTGACCGAC TACCACATCG ATCAAGTATC CAATTTAGTT GAGT

44

(2) INFORMATION FOR SEQ ID NO:61:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 44 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(A) DESCRIPTION: /desc = "primer KE135A28"

(iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:61:

ACTCAACTAA ATTGGATACT TGATCGATGT GGTAGTCGGT CACG

44

(2) INFORMATION FOR SEQ ID NO:62:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 37 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: other nucleic acid
 - (A) DESCRIPTION: /desc = "primer KE136A28"

(iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:62:

GCAGATCTGA GCTCTTAGGT ACCCAATAGC GTAACGT

37

(2) INFORMATION FOR SEQ ID NO:63:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 21 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: other nucleic acid
 - (A) DESCRIPTION: /desc = "primer KE137A28"

(iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:63:

GCTGATTATG CATCAGCCTA T

21

(2) INFORMATION FOR SEQ ID NO:64:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 38 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: other nucleic acid
 - (A) DESCRIPTION: /desc = "primer KE138A28"

(iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:64:

GCAGATCTGA GCTCTTATTC CTCCATAAGA AGTAATTC

38

(2) INFORMATION FOR SEQ ID NO:65:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 23 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: other nucleic acid
 - (A) DESCRIPTION: /desc = "primer MK05A28"
- (iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:65:

CAAAGGTACC CAATAGCGTA ACG

23

(2) INFORMATION FOR SEQ ID NO:66:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: other nucleic acid
 - (A) DESCRIPTION: /desc = "primer MK35A28"
- (iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:66:

AACGAGGTGT ACATCGACCG

20

(2) INFORMATION FOR SEQ ID NO:67:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 42 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: other nucleic acid
 - (A) DESCRIPTION: /desc = "forward primer for pCIB4434"
- (iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:67:

GCACCGATAT CACCATCCAA GGAGGCGATG ACGTATTCAA AG

42

(2) INFORMATION FOR SEQ ID NO:68:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 51 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid
(A) DESCRIPTION: /desc = "reverse primer for pCIB4434"

(iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:68:

AGCGCATCGA TTCGGCTCCC CGCACTTGCC GATTGGACTT GGGGCTGAAA G

51

(2) INFORMATION FOR SEQ ID NO:69:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 30 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid
(A) DESCRIPTION: /desc = "primer #1"

(iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:69:

ATTACGTTAC GCTATTGGGT ACCTTTGATG

30

(2) INFORMATION FOR SEQ ID NO:70:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 98 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid
(A) DESCRIPTION: /desc = "primer #2"

(iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:70:

TCCCCGTCCC TGCAGCTGCA GTCTAGGTCC GGGTTCCACT CCAGGTGCGG AGCGCATCGA

60

TTCGGCTCCC CGCACTTGCC GATTGGACTT GGGGCTGA

98

(2) INFORMATION FOR SEQ ID NO:71:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 98 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

- (A) DESCRIPTION: /desc = "primer #3"

(iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:71:

CAAGTGC GGG GAGCCGAATC GATGCGCTCC GCACCTGGAG TGGAACCCGG ACCTAGACTG

60

CAGCTGCAGG GACGGGGAAA AATGTGCCCA TCATTCCC

98

(2) INFORMATION FOR SEQ ID NO:72:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 30 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

- (A) DESCRIPTION: /desc = "primer #4"

(iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:72:

TGGTTTCTCT TCGAGAAATT CTAGATTTC

30

(2) INFORMATION FOR SEQ ID NO:73:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 24 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

- (A) DESCRIPTION: /desc = "primer used to map transcriptional start site for TrpA gene"

(iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:73:

CCGTTCGTTTC CTCCTTCGTC GAGG

24

(2) INFORMATION FOR SEQ ID NO:74:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 26 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(v) FRAGMENT TYPE: N-terminal

(ix) FEATURE:

- (A) NAME/KEY: Peptide
- (B) LOCATION: 1..26
- (D) OTHER INFORMATION: /note= "N-terminal peptide from pollen specific protein"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:74:

Thr	Thr	Pro	Leu	Thr	Phe	Gln	Val	Gly	Lys	Gly	Ser	Lys	Pro	Gly	His
1				5					10					15	
Leu	Ile	Leu	Thr	Pro	Asn	Val	Ala	Thr	Ile						
			20					25							

(2) INFORMATION FOR SEQ ID NO:75:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(v) FRAGMENT TYPE: internal

(ix) FEATURE:

- (A) NAME/KEY: Peptide
- (B) LOCATION: 1..20
- (D) OTHER INFORMATION: /note= "internal peptide of pollen specific protein"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:75:

Lys	Pro	Gly	His	Leu	Ile	Leu	Thr	Pro	Asn	Val	Ala	Thr	Ile	Ser	Asp
1				5					10					15	

Val Val Ile Lys
20

(2) INFORMATION FOR SEQ ID NO:76:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 16 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
- (iii) HYPOTHETICAL: NO
- (v) FRAGMENT TYPE: internal
- (ix) FEATURE:
 - (A) NAME/KEY: Peptide
 - (B) LOCATION: 1..16
 - (D) OTHER INFORMATION: /note= "internal peptide from pollen specific protein"
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:76:

Ser	Gly	Gly	Thr	Arg	Ile	Ala	Asp	Asp	Val	Ile	Pro	Ala	Asp	Phe	Lys
1				5					10					15	

(2) INFORMATION FOR SEQ ID NO:77:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 12 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
- (iii) HYPOTHETICAL: NO
- (v) FRAGMENT TYPE: internal
- (ix) FEATURE:
 - (A) NAME/KEY: Peptide
 - (B) LOCATION: 1..12
 - (D) OTHER INFORMATION: /note= "internal peptide from pollen specific protein"
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:77:

Glu	His	Gly	Gly	Asp	Asp	Phe	Ser	Phe	Thr	Leu	Lys
1				5					10		

(2) INFORMATION FOR SEQ ID NO:78:

- (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 12 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(v) FRAGMENT TYPE: internal

(ix) FEATURE:

- (A) NAME/KEY: Peptide
- (B) LOCATION: 1..12
- (D) OTHER INFORMATION: /note= "internal peptide from pollen specific protein"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:78:

Glu	Gly	Pro	Thr	Gly	Thr	Trp	Thr	Leu	Asp	Thr	Lys
1				5					10		

(2) INFORMATION FOR SEQ ID NO:79:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

- (A) DESCRIPTION: /desc = "oligonucleotide #51"

(iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:79:

AARTCRTCAB CACCRTGYTC

20

(2) INFORMATION FOR SEQ ID NO:80:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 17 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

- (A) DESCRIPTION: /desc = "oligonucleotide #58"

(iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:80:

CCYTTNCCCA CYTGRAA

17

(2) INFORMATION FOR SEQ ID NO:81:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 33 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: other nucleic acid
 - (A) DESCRIPTION: /desc = "oligonucleotide PE51"
- (iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:81:

TGGCCCATGG CTGCGGCGGG GAACGAGTGC GGC

33

(2) INFORMATION FOR SEQ ID NO:82:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 40 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: other nucleic acid
 - (A) DESCRIPTION: /desc = "primer #42"
- (iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:82:

AGCGGTCGAC CTGCAGGCAT GCGATCTGCA CCTCCCGCCC

40

(2) INFORMATION FOR SEQ ID NO:83:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 18 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: other nucleic acid
 - (A) DESCRIPTION: /desc = "primer #43"
- (iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:83:

ATGGGCAAGG AGCTCGGG

18

(2) INFORMATION FOR SEQ ID NO:84:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 21 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: other nucleic acid
 - (A) DESCRIPTION: /desc = "primer #SK50"
- (iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:84:

CCCTCAAAA TCTAGAAACC T

21

(2) INFORMATION FOR SEQ ID NO:85:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 27 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: other nucleic acid
 - (A) DESCRIPTION: /desc = "primer #SK49"
- (iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:85:

TAATGTCGAC GAACGGCGAG AGATGGA

27

(2) INFORMATION FOR SEQ ID NO:86:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 22 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: other nucleic acid
 - (A) DESCRIPTION: /desc = "primer KE99A28"
- (iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:86:

TGCGGTTACC GCCGATCACA TG

22

(2) INFORMATION FOR SEQ ID NO:87:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 41 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: other nucleic acid
 - (A) DESCRIPTION: /desc = "primer KE97A28"
- (iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:87:

GCGGTACCGC GTCGACGCGG ATCCCGCGGC GGAAGCTAA G

41

(2) INFORMATION FOR SEQ ID NO:88:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 16 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: other nucleic acid
 - (A) DESCRIPTION: /desc = "primer KE100A28"
- (iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:88:

GTCGTCGACC GCAACA

16

(2) INFORMATION FOR SEQ ID NO:89:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 39 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: other nucleic acid
 - (A) DESCRIPTION: /desc = "primer KE98A28"
- (iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:89:

GCGGTACCGC GTTAACGCGG ATCCTGTCCG ACACCGGAC

39

(2) INFORMATION FOR SEQ ID NO:90:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: other nucleic acid
 - (A) DESCRIPTION: /desc = "primer KE104A28"

(iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:90:

GATGTCGTCG ACCGCAACAC

20

(2) INFORMATION FOR SEQ ID NO:91:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 35 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: other nucleic acid
 - (A) DESCRIPTION: /desc = "primer KE103A28"

(iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:91:

GCGGTACCGC GGATCCTGTC CGACACCGGA CGGCT

35

(2) INFORMATION FOR SEQ ID NO:92:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 26 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: other nucleic acid
 - (A) DESCRIPTION: /desc = "primer KE127"

(iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:92:

GCGGATCCGG CTGCGGCGGG GAACGA

26

(2) INFORMATION FOR SEQ ID NO:93:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 23 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: other nucleic acid
 - (A) DESCRIPTION: /desc = "primer KE150A28"
- (iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:93:

ATTTCGCATGC ATGTTTCATT ATC

23

(2) INFORMATION FOR SEQ ID NO:94:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 37 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: other nucleic acid
 - (A) DESCRIPTION: /desc = "primer KE151A28"
- (iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:94:

GCTGGTACCA CGGATCCGTC GCTTCTGTGC AACAACC

37